

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:26:58 ; Search time 10.93 Seconds
(without alignments)
239.825 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171
Sequence: 1 MASQKRPQSGHSGSKYLATAS.....SKIFKLGGRDSHSGSPMARR 171

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 152396 seqs, 15329161 residues

Word size : 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents,AA:*

- 1: /cgnl_7/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgnl_7/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgnl_7/prodata/1/1aa/6_COMB.pep:*
- 4: /cgnl_7/prodata/1/1aa/PCRTUS_COMB.pep:*
- 5: /cgnl_7/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	171	2	US-08-781-122-2
2	170	99.4	170	2	US-08-327-357A-1
3	63	36.8	168	5	5194425-4
4	41	24.0	170	1	US-08-227-372-1
5	41	24.0	170	3	US-08-470-397-1
6	41	24.0	170	5	5194425-3
7	40	23.4	40	3	US-08-297-395-2
8	26	15.2	170	5	5468481-3
9	24	14.0	24	2	US-08-480-190-46
10	24	14.0	24	2	US-08-468-379-46
11	24	14.0	24	4	PCT-US93-07545-46
12	23	13.5	23	1	US-08-787-547-1
13	21	12.3	21	1	US-08-787-547-33
14	20	11.7	20	1	US-08-227-372-4
15	20	11.7	20	1	US-08-787-547-34
16	20	11.7	20	1	US-08-787-547-35
17	20	11.7	20	1	US-08-787-547-40
18	20	11.7	20	2	US-08-640-344-6
19	20	11.7	20	2	US-08-640-344-8
20	20	11.7	20	2	US-08-640-344-9
21	20	11.7	20	2	US-08-468-540B-1
22	20	11.7	20	2	US-08-468-540B-2
23	20	11.7	20	2	US-08-468-540B-4
24	20	11.7	20	2	US-08-468-540B-5
25	20	11.7	20	2	US-08-468-540B-10
26	20	11.7	20	2	US-08-468-540B-11
27	20	11.7	20	2	US-08-468-540B-13
28	20	11.7	20	2	US-08-606-639A-5

29	20	11.7	20	3	US-08-470-397-4	Sequence 4, Appl
30	20	11.7	20	3	US-08-297-395-14	Sequence 14, Appl
31	20	11.7	20	3	US-08-297-395-15	Sequence 15, Appl
32	20	11.7	20	3	US-08-297-395-16	Sequence 16, Appl
33	20	11.7	20	3	US-08-297-395-17	Sequence 17, Appl
34	20	11.7	20	3	US-08-297-395-18	Sequence 18, Appl
35	20	11.7	20	3	US-08-297-395-19	Sequence 19, Appl
36	20	11.7	20	3	US-08-297-395-20	Sequence 20, Appl
37	20	11.7	20	3	US-08-297-395-21	Sequence 21, Appl
38	20	11.7	20	3	US-08-297-395-22	Sequence 22, Appl
39	20	11.7	20	3	US-08-297-395-23	Sequence 23, Appl
40	20	11.7	20	3	US-08-297-395-25	Sequence 25, Appl
41	19	11.1	19	2	US-08-640-344-2	Sequence 2, Appl
42	19	11.1	19	2	US-08-468-540B-9	Sequence 9, Appl
43	19	11.1	19	2	US-08-468-540B-12	Sequence 12, Appl
44	19	11.1	19	3	US-08-297-395-1	Sequence 1, Appl
45	19	11.1	19	3	US-08-297-395-24	Sequence 24, Appl

ALIGNMENTS

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RESULT 1
US-08-781-122-2
; Sequence 2, Application US/08781122
; Patent No. 5948764
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; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
; TITLE OF INVENTION: UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,122
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Markl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-122-2

Query Match 100.0%; Score 171; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 4e-160;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASQKRPQSGHSGSKYLATASMDHARGFLPRHRDGIIDISIGRFGDGGAKRGSGKD 60
Db 1 MASQKRPQSGHSGSKYLATASMDHARGFLPRHRDGIIDISIGRFGDGGAKRGSGKD 60
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Qy	61	SHHARATHTHSLSQKSHSGRTQDENPVVHFEKNTVTRTPPPSGKGRGLSTLRFSGAE	120
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Qy	121	GORGFGVGRASDYKSAHKFEKLVNDQGLSTKFTKLGAGDSRSGSMAR	171
Db	121	GORGFGVGRASDYKSAHKFEKLVNDQGLSTKFTKLGAGDSRSGSMAR	171

RESULT 2
US-08-327-357A-1
; Sequence 1, Application US/08327357A
; Patent No. 5817629

GENERAL INFORMATION:
APPLICANT: WARREN, Kenneth G.
APPLICANT: Catz, Ingrid
TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC
TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESS: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: USA

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: FILING DATE: 21-OCT-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/798,099
: FILING DATE: 27-NOV-1991
: PRIOR APPLICATION DATA:
:
:

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APPLICATION NUMBER: CA 2,053,799-0
FILING DATE: 22-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 27052-115466
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-6810
TELEFAX: 202-962-8300

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; INFORMATION FOR SEQ ID NO: 1
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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 170 amino acids
;   TYPE: amino acid
;   COMPLETENESS:

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

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; ORGANISM: Homo sapiens
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; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
;
US-08-327-357A-1

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Query Match	99.4%	Score 170;	DB 2;	Length 170;
Best Local Similarity	100.0%	Pred. No. 3.8e-159;		
Matches 170;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 2 ASOKRPSORHSSKTLATSTMDHARRHGRLPHNRDTGLDSTGREFGDDRAPKRGSGKDS 61
Db 1 ASOKRPSORHSSKTLATSTMDHARRHGRLPHNRDTGLDSTGREFGGGRGAPKRGSGKDS 60
QY 62 HHPARTAHGSLPOKSHGRTODENPVVHEFFKNIVTPRTPPSOGKGRGLSIRFSWGAEG 121

Db 61 HHPARTAHYGLLPKSKSGRGRDNDPEVYHFKNKTYTPPTPPPSQCKGKGLSLSLFSSMCAG 120

Qy 122 QRPFGYGGRASDYKSAHKFGKGYDAQGLTSLIKFLGGRDSRSGSPARR 171
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Db 121 QRPFGYGGRASDYKSAHKFGKGYDAQGLTSLIKFLGGRDSRSGSPARR 170
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RESULT 3
5194425-4

PATENT NO. 5194425
 APPLICANT: SHARMA, SOMESE D.; LERCH, L. BERNARD; CLARK, BRIAN R.
 TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN AMELIORATING AUTOIMMUNITY

NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/367,751
FILING DATE: 21-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988

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;SEQ ID NO:4:
;      LENGTH: 168
5194425-4

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Query Match	36.8%	Score 63	DB 5	Length 168
Best Local Similarity	100.0%	Pred. No.	2.1e-54	
Matches 63, Conservative	0	Mismatches	0	Indels 0; Gaps 0

QY 109 GLSLRFSWAEGRPRGFGYGGRASDYKSAHKFKGVDAQGLSKLIFKLGRDSRRGSPM 168
|||
Db 106 GLSLRFSWAEGRPRGFGYGGRASDYKSAHKFKGVDAQGLSKLIFKLGRDSRRGSPM 165

Qy	169	ARR	171
Db	166	ARR	168

RESULT 4
US-08-227-372-1
; Sequence 1, Application US/08227372
; Patent No. 5763585
GENERAL INFORMATION:

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1  GENERAL INFORMATION:
2  APPLICANT: Nag, Bishwajit
3  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
4  TITLE OF INVENTION: MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
5  NUMBER OF SEQUENCES: 4
6  CORRESPONDENCE ADDRESS:
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```

ADDRESS: Townsend and Townsend Kourie and C
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California

```

;      COUNTRY:  US
;      ZIP:      94105-1493
;      COMPUTER READABLE
;      MEDIUM TYPE:  F1
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216

ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..170
OTHER INFORMATION: /note= "Myelin basic protein"
US-08-227-372-1

Query Match 24.0%; Score 41; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.1e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 QDENPVVHFFKNIVTPRPPSGKGRGLSRSFSGAEGQ 122
Db 81 QDENPVVHFFKNIVTPRPPSGKGRGLSRSFSGAEGQ 121

RESULT 5
US-08-470-397-1
Sequence 1, Application US/08470397
Patent No. 6007820
GENERAL INFORMATION:
APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: Purification and Characterization of
TITLE OF INVENTION: MHC-peptide Complexes Useful in Ameliorating Autoimmunity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,397
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,372
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1

OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = N-acetyl-alanine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Ala or absent"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Arg or His"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Ser or Gly"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Ser or Thr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 40
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Leu or Ile"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 46
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Ser or Gly"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 59
OTHER INFORMATION: /product= "OTHER"
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 66
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Thr or Ala"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 75
OTHER INFORMATION: /product= "OTHER"
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 76
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Gln or absent"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 80
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Pro or Thr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 141
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Leu or Phe"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 144
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = His or Val"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..170
OTHER INFORMATION: /note= "Myelin basic protein"
US-08-470-397-1

Query Match 24.0%; Score 41; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.1e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSGAGEQ 122
DB 81 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSGAGEQ 121

RESULT 6
5194425-3
; Patent No. 5194425
; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
; BRIAN R.
; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
; AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/367,751
; FILING DATE: 21-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; SEQ ID NO:3:
; LENGTH: 170
5194425-3

Query Match 24.0%; Score 41; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.1e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSGAGEQ 122
DB 81 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSGAGEQ 121

RESULT 7
US-08-297-395-2
; Sequence 2, Application US/08297395A
; Patent No. 6039947
; GENERAL INFORMATION:
; APPLICANT: Howard L. Weiner
; APPLICANT: David A. Hailer
; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
; FILE REFERENCE: 1010/05723US3
; CURRENT APPLICATION NUMBER: US/08/297,395A
; CURRENT FILING DATE: 1994-08-11
; EARLIER APPLICATION NUMBER: 08/059,189
; EARLIER FILING DATE: 1993-05-06
; EARLIER APPLICATION NUMBER: 07/502,559
; EARLIER FILING DATE: 1990-03-30
; EARLIER APPLICATION NUMBER: PCT/US88/02139
; EARLIER FILING DATE: 1988-06-24
; EARLIER APPLICATION NUMBER: 07/065,734
; EARLIER FILING DATE: 1987-06-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-297-395-2

Query Match 23.4%; Score 40; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 SLPOKSHGRTQDENPVHFEKNTVPTPTPPSGKRGSL 111
DB 51 SLPOKSHGRTQDENPVHFEKNTVPTPTPPSGKRGSL 111

DB 1 SLPOKSHGRTQDENPVHFEKNTVPTPTPPSGKRGSL 40

RESULT 8
5468481-3
; Patent No. 5468481
; APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L.
; TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL
; IN AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,293
; FILING DATE: 14-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 690,840
; FILING DATE: 23-APR-1991
; APPLICATION NUMBER: 576,084
; FILING DATE: 30-AUG-1990
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; APPLICATION NUMBER: 635,840
; FILING DATE: 28-DEC-1998
; APPLICATION NUMBER: 367,751
; FILING DATE: 21-JUN-1989
; SEQ ID NO:3:
; LENGTH: 170
5468481-3

Query Match 15.2%; Score 26; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.4e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 DAQGLSKIFKLGGRDSRSGSPMAR 171
DB 145 DAQGLSKIFKLGGRDSRSGSPMAR 170

RESULT 9
US-08-480-190-46
; Sequence 46, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Darlo A. A. Vignelli
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-46

Query Match 14.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 5,4e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRQDENPVVHFFKNIVTPRTPP 102
Db 1 GRQDENPVVHFFKNIVTPRTPP 24

RESULT 10
US-08-488-379-46
Sequence 46, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-488-379-46

Query Match 14.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 5,4e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRQDENPVVHFFKNIVTPRTPP 102
Db 1 GRQDENPVVHFFKNIVTPRTPP 24

RESULT 11
PCT-US93-07545-46
Sequence 46, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-46

Query Match 14.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5,4e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRQDENPVVHFFKNIVTPRTPP 102
Db 1 GRQDENPVVHFFKNIVTPRTPP 24

RESULT 12
US-08-787-547-1
Sequence 1, Application US/08787547
Patent No. 5783567

```

GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-1

Query Match      13.5%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRTODENPVVHFKNVTPTTP 101
DB 1 GRTODENPVVHFKNVTPTTP 23

RESULT 13
US-08-787-547-33
Sequence 33, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-33

Query Match      12.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SQRHGSKYLASTMDHARG 28
DB 1 SQRHGSKYLASTMDHARG 21

RESULT 14
US-08-227-372-4
Sequence 4, Application US/08227372
Patent No. 5763585
GENERAL INFORMATION:
APPLICANT: Ng, Bishwajit
TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
```

TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-227-372-4

Query Match 11.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GFGYGRASDYKSAHKFGK 144
|||||
Db 1 GFGYGRASDYKSAHKFGK 20

RESULT 15

US-08-787-547-34
Sequence 34, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-34

Query Match 11.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 RDTGILDSIGRFFGGDRGAP 53
|||||
Db 1 RDTGILDSIGRFFGGDRGAP 20

Search completed: September 26, 2000, 19:36:55
Job time: 597 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:26:53 ; Search time 11.86 Seconds

(Without alignments)
341.511 Million cell updates/sec

Title: US-09-218-277-12

Sequence: 1 MASQKRPSQRHSGSKYLATAS.....SKIFKLGRDSRSGSPMARR 171

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 188963 seqs, 23686106 residues

Word size : 0

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	171	1	R97627 Human myelin basic
2	171	100.0	171	1	R99580 Human myelin basic
3	170	99.4	170	1	R48592 Human myelin basic
4	170	99.4	170	1	R95406 Myelin oligodendro
5	113	66.1	197	1	W00309 Human myelin basic
6	113	66.1	203	1	W06107 Foetal myelin basi
7	113	66.1	203	1	W06108 Human myelin basi
8	113	66.1	373	1	W06103 MP4 chimera (MBP21
9	113	66.1	375	1	W06104 PM4 chimera (delta
10	113	66.1	385	1	W06102 MP3 chimera (MBP21
11	113	66.1	492	1	W06105 M0G0P4 chimera (MB
12	92	53.8	170	1	R30736 Human MBP. Pure ma
13	86	50.3	170	1	R35440 Human basic myelin
14	63	36.8	168	1	R04717 Empirically determ
15	46	26.9	46	1	W72360 Human myelin basic
16	46	26.9	167	1	R48595 Human myelin basic
17	45	26.3	127	1	R48596 Rat myelin basic p
18	45	26.3	168	1	R48594 Rabbit myelin basi
19	41	24.0	170	1	R02226 Myelin basic prote
20	41	24.0	170	1	R30735 Bovine MBP. Pure m
21	41	24.0	170	1	R45947 Myelin basic prote
22	41	24.0	170	1	W57236 Myelin basic prote
23	33	19.3	169	1	R48593 Cattle myelin basi
24	32	18.7	32	1	R85138 Human MBP residues
25	32	18.7	32	1	R95369 Residues 139-170 o
26	27	15.8	27	1	R95372 Residues 142-168 o
27	26	15.2	170	1	R86422 Myelin basic prote
28	25	14.6	25	1	R85135 Human MBP residues
29	25	14.6	25	1	R95371 Residues 142-166 o
30	25	14.6	25	1	R95367 Residues 111-135 o
31	25	14.6	25	1	R95342 MBP-2.5 (80-104).
32	25	14.6	25	1	R95346 MBP-4 (141-165). M
33	25	14.6	25	1	R95347 MBP-5 (101-125). M

34	25	14.6	25	1	W43948 Human myelin basic
35	25	14.6	25	1	W43952 Human myelin basic
36	25	14.6	25	1	W43953 Human myelin basic
37	24	14.0	24	1	R49336 Myelin basic prote
38	24	14.0	24	1	MBP-2.1 (82-105).
39	24	14.0	24	1	R74158 Antigenic peptide
40	24	14.0	24	1	W37554 Human myelin basic
41	24	14.0	24	1	W54719 Peptide from myel
42	23	13.5	23	1	R85137 Human MBP residues
43	23	13.5	23	1	R95339 MBP-2.2 (82-104).
44	23	13.5	23	1	R95343 MBP-2.6 (80-102).
45	23	13.5	23	1	R95337 MBP-2 (83-105). My

ALIGNMENTS

RESULT 1	
R97627	1
ID	R97627 standard; Protein; 171 AA.
AC	R97627;
DT	09-NOV-1996 (first entry)
DE	Human myelin basic protein.
KW	Myelin basic protein; MBP; multiple sclerosis; MS; treatment; prevention; analogue.
OS	Homo sapiens.
FT	Key
FM	Location/Qualifiers
FF	peptide 86..99
FN	/Label- Claimed peptide region.
PD	W0616085-A1.
PF	30-MAY-1996.
PR	16-NOV-1995; U14402.
PS	18-NOV-1994; US-342078.
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.
PI	(STRD) UNIV STANFORD MEDICAL CENT.
DR	Conlon PJ, Gaur A, Ling N, Steinman L;
DR	WPI; 96-268534/27.
DR	N-PSDB; T30269.
PT	Peptide analogue of human myelin basic protein - has lysine 91
PS	Replaced by another amino acid, useful to treat multiple sclerosis
CC	Claim 1: Figure 1: 30pp: English.
CC	A peptide analogue comprising amino acids 87-99 of human myelin
CC	basic protein (MBP), where lys91 is substituted for another amino
CC	acid can be used to treat and prevent multiple sclerosis. The
CC	peptide analogue is administered at a dosage range of 5-50 mg/kg.
Sequence	171 AA;
Query Match	100.0%; Score 171; DB 1; Length 171;
Best Local Similarity	100.0%; Pred. No. 5,7e-161;
Matches 171; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MASQKRPSQRHSGSKYLATASMDHARHGFPRHDTGLDSTGRFGGDRAPKRGSKD 60
DB	1 MASQKRPSQRHSGSKYLATASMDHARHGFPRHDTGLDSTGRFGGDRAPKRGSKD 60
OY	61 SHHPRATHYGSILPKSHGRGTODENPVVHFPPKNITPTPTPPSOGKGLSRSFSGAE 120
DB	61 SHHPRATHYGSILPKSHGRGTODENPVVHFPPKNITPTPTPPSOGKGLSRSFSGAE 120
OY	121 GORPEFGYGRASDYKSAHKGFGVDAQGLTSKIFKLGRDSRSGSPMARR 171
DB	121 GORPEFGYGRASDYKSAHKGFGVDAQGLTSKIFKLGRDSRSGSPMARR 171
RESULT 2	
R99580	
ID	R99580 standard; Protein; 171 AA.
AC	R99580;
DT	07-NOV-1996 (first entry)
DE	Human myelin basic protein (MBP).
KW	Myelin basic protein; MBP; multiple sclerosis; MS; competition; inhibition; major histocompatibility complex; MHC; thymocyte; T cell;

KW experimental allergic encephalomyelitis; EAE; analogue.
OS Homo sapiens.
PN MO9616086-A1.
PD 30-MAY-1996.
PE 16-NOV-1995; U14403.
PR 18-NOV-1994; US-342408.
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
PI Conlon PJ, Gaur A, Ling N, Steilman L;
DR WPI; 96-268535/27.
PT Peptide analogues of human myelin basic protein - useful for
PS treatment of multiple sclerosis
PS Disclosure: Figure 1, 61pp; English.
CC Peptide analogues comprising at least seven amino acids from
CC residues 86-99 of human myelin basic protein (MBP), can be used to
CC treat multiple sclerosis by competing for the binding of native MBP
CC peptide to MHC and by not causing proliferation of an MBP reactive T-
CC cell line. The peptide analogues also inhibit the induction of
CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.
CC The peptide analogues have a reduced susceptibility to proteolysis
CC in vivo.
SQ Sequence 171 AA;

Query Match 100.0%; Score 171; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 5.7e-161;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGDGAAPRSGSKD 60
DB 1 MASQRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGDGAAPRSGSKD 60

QY 61 SHHPARTAHYGSLPQKSHGRTODENPVHFEKNIIVTPRTPPQSGKRGSLSRFSWGAE 120
DB 61 SHHPARTAHYGSLPQKSHGRTODENPVHFEKNIIVTPRTPPQSGKRGSLSRFSWGAE 120

QY 121 GQRGFGYGGRASDYKSAHKGFGVDAQGTLTKIFKLGSDSRSGSPMARR 171
DB 121 GQRGFGYGGRASDYKSAHKGFGVDAQGTLTKIFKLGSDSRSGSPMARR 171

RESULT 3
R48592
ID R48592 standard; protein: 170 AA.
AC R48592;
DE 31-JUL-1994 (first entry)
KW Human myelin basic protein.
KM Proteolipid protein; myelin basic protein; retrovirus;
KM neurological disease; by-stander antigen; TGF-beta;
KM transforming growth factor-beta; T-cell; T-lymphocyte;
KM myelopathy; paraparesis; human immunodeficiency virus type 1.
OS Homo sapiens.
PN MO9404121-A.
PD 03-MAR-1994.
PE 17-AUG-1993; U07786.
PR 17-AUG-1992; US-931217.
PA (AUTO-) AUTOIMMUNE INC.
PI Hafler DA, Weiner HL;
DR WPI; 94-082786/10.
PT Treating retroviral associated neurological disease - by admin.
PT factor of by-stander antigen, causing release of transforming growth
PS factor beta from suppressor T cells
PS Disclosure: Page 49; 64pp; English.
CC Myelin basic proteins (sequences R48592-96) and cattle proteolipid
CC protein (R48592) elicit the release of TGF-beta from suppressor T-
CC cells and target the T-cells to neural tissue under cytotoxic
CC attack, thereby reducing neurological disease, e.g. HTLV-1
CC associated myelopathy, tropical spastic paraparesis and HIV
CC infection.
SQ Sequence 170 AA;

Best Local Similarity 100.0%; Pred. No. 5.5e-160;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGDGAAPRSGSKD 61
DB 1 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGDGAAPRSGSKD 60

QY 62 HHPARTAHYGSLPQKSHGRTODENPVHFEKNIIVTPRTPPQSGKRGSLSRFSWGAE 121
DB 62 HHPARTAHYGSLPQKSHGRTODENPVHFEKNIIVTPRTPPQSGKRGSLSRFSWGAE 120

QY 122 GQRGFGYGGRASDYKSAHKGFGVDAQGTLTKIFKLGSDSRSGSPMARR 171
DB 122 GQRGFGYGGRASDYKSAHKGFGVDAQGTLTKIFKLGSDSRSGSPMARR 170

RESULT 4
R95406
ID R95406 standard; protein: 170 AA.
AC R95406;
DE 16-DEC-1996 (first entry)
KW Myelin oligodendrocyte protein.
KM Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
KM CD4+, T-cell; autoimmune disease; demyelination; central nervous system;
KM CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
KM relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
KM diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
KM psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
KM myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
OS Homo sapiens.
PN MO9612737-A2.
PD 02-MAY-1996.
PE 25-OCT-1995; U13682.
PR 25-OCT-1994; US-328224.
PR 15-MAR-1995; US-404228.
PR 25-OCT-1995; ZA-009033.
PA (IMMU-) IMMULOGIC PHARM CORP.
PI Devaux B, Franzen H, Hsu D, Pallard X;
PI Rothbard J, Samsen M, Shi J, Smlek D;
DR WPI; 96-230552/23.
PT Myelin basic derived peptide(s) and analogs - used in the treatment
PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
PS Example 9; Fig 1, 91pp; English.
CC This sequence represents the human myelin oligodendrocyte protein (MOG).
CC Immunisation with MOG (or the peptide fragments shown in R95375-R95385)
CC can be used to induce experimental allergic encephalomyelitis (EAE) in
CC susceptible strains of mice. EAE is a CD4+ T-cell mediated autoimmune
CC disease which results in demyelination of the central nervous system,
CC resulting in paralysis and other neurological abnormalities. EAE is a
CC commonly used animal model for human multiple sclerosis (MS). These
CC sequences can be used in compositions for treating MS in a mammal. The
CC composition acts to down regulate the autoimmune response, and may be
CC administered in an amount sufficient to prevent the onset of symptoms of
CC MS. The compositions may also be used to treat advanced stage MS,
CC especially relapsing-remitting MS, chronic progressive MS or benign MS.
CC These peptides may also be used in the treatment of other diseases
CC involving myelin autoantigens, including diabetes, Graves disease,
CC myasthenia gravis, Good Pasture's syndrome, psoriasis, thyroiditis, and
CC rheumatoid arthritis. Peptides derived from other myelin autoantigens,
CC such as myelin basic protein (MBP, see R95334-R95374) proteolipid
CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as
CC alternatives to the MOG peptides in these compositions.
SQ Sequence 170 AA;

Query Match 99.4%; Score 170; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 5.5e-160;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGDGAAPRSGSKD 61
DB 1 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGDGAAPRSGSKD 60

OY	62	HHPARTATAYGSLPKSHRRTODENPVVHFFKNITYTPRPSPSGKGGGLSLSRSSNAEG	120
Dd	61	HHPATATAYGSLPKSKHRGTODENPVVHFFKNITYTPRPSPSGKGGGLSLSRFSWGAEG	120
OY	122	QRPFGYGGRASDYKSAHKGFKGVDAGTLSKIFPLGGRRDSRSSGPAPARR	171
Dd	121	QRPFYGIGRASDYSKSAHKGFKGVDAGTLSKIFKLGGRRDSRSSGPAPARR	170
RESULT	5		
ID	M00399	standard; Protein; 197 AA.	
AC	M00399	(first entry)	
DT	01-FEB-1997		
DE	Human myelin basic protein [foetal isoform].		
KW	Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;		
KM	multiple sclerosis; autoimmune disease; diagnosis; therapy;		
KW	T-lymphocyte; T-cell; anergy; apoptosis.		
OS	Homo sapiens.		
FH	Key	Location/qualifiers	
FT	region	60..85	
FT	/label= x2		
FT	/note= "exon 2-encoded region"		
misc_difference	81	/note= "Cys-81 may be replaced by any standard amino acid, esp. an uncharged amino acid of mol.wt. below about 150, partic. Ser, in constructs of the invention"	
PD	WC0634622-A1.		
PF	07-NOV-1996.		
PR	22-APR-1996; U05611.		
PR	02-MAY-1995; US-431648.		
PR	02-MAY-1995; US-431644.		
PR	07-JUN-1995; US-482114.		
PA	(ALEX-) ALEXON PHARM INC.		
PA	(USSH -) DEPT HEALTH & HUMAN SERVICES.		
PI	Lemario MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;		
PI	Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;		
DR	WPI; 96-505989/50.		
DR	N-PDB: T41889.		
PT	New human myelin basic protein and proteolipid protein variant(s) -		
PT	used in the assessment, diagnosis and treatment of multiple		
PT	sclerosis		
PS	Claim 1; Page 79-80; 156pp; English.		
CC	The native human 21.5 kDa foetal isoform (M00399) of myelin basic		
CC	protein, MBP-X2Cys81, includes an exon 2-encoded region (x2) that		
CC	may contain an epitope involved in the pathogenesis of multiple		
CC	sclerosis (MS); the X2 region is not found in the MBP of healthy		
CC	adults. Recombinant MBP-X2, or variants modified to improve		
CC	bacterial expression (see also W06107), can be produced in a		
CC	large scale in bacterial hosts. They are useful for assaying		
CC	T-cells for responsiveness to MBP epitopes and can be used as		
CC	therapeutic agents that act by inducing T-cell responses,		
CC	including energy and apoptosis, as a means of treating MS.		
SQ	Sequence 197 AA;		
Query Match	66.1%; Score 113; DB 1; Length 197;		
Best Local Similarity	100.0%; Pred. No. 7.9e-104;		
Matches 113; Conservative	0; Mismatches 0; Indels 0; Gaps		
OY	59	KDSHHPARTATAYGSLPKSHRGTODENPVVHFFKNITYTPRPSPSGKGGGLSLSRFSWG	118
Dd	85	KDSHHPARTATAYGSLPKSHRGTODENPVVHFFKNITYTPRPSPSGKGGGLSLSRFSWG	144
OY	119	AEGORPGFYGYGRASDYKSAHKGFKGVDAGTLSKIFKLGGRRDSRSSGPAPARR	171
Dd	145	AEGORPGFYGYGRASDYKSAHKGFKGVDAGTLSKIFKLGGRRDSRSSGPAPARR	197
RESULT	6		
ID	W06107	standard; Protein; 203 AA.	

AC	W06107;		(first entry)	
DE	01-FEB-1997			
DT	Foetal myelin basic protein MBP-X2Cys81/bact.			
KV	Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;			
KW	multiple sclerosis; autoimmune disease; diagnosis; therapy;			
KM	T-lymphocyte; T-cell; anergy; apoptosis.			
OS	Synthetic.			
FH	Key	Location/Qualifiers		
FT	region	60..85	/label= X2	
FT		/note= "exon 2-encoded region"		
PN	W09634622-A1.			
PD	07-NOV-1996.			
PF	22-APR-1996; U05611.			
PR	02-MAY-1995; US-431648.			
PR	02-MAY-1995; US-431648.			
PR	07-JUN-1995; US-482114.			
PA	(ALEX-) ALEXION PHARM INC.			
PA	(UEXH) US DEPT HEALTH & HUMAN SERVICES.			
PI	Lienardo MJ, Mats L, McFarland HF, Mueller EE, Mueller JP;			
PI	Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;			
DR	WPI: 96-505898/50.			
DR	N-PDSB: T41896.			
PT	New human myelin basic protein and proteolipid protein variant(s) -			
PT	used in the assessment, diagnosis and treatment of multiple			
PT	sclerosis			
PS	Disclosure: Page 81-82; 156pp. English.			
CC	A 21.5 kDa foetal isoform (W06107) of myelin basic protein,			
CC	MBP+X2Cys81/bact., is the product of a DNA construct (T41896)			
CC	based on the human foetal MBP+X2Cys81 isoform (W00399) but			
CC	utilising bacterially-preferred codons in place of the native human			
CC	codons (see also T41889). This increases prodn. of the msp in E.			
CC	coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also			
CC	W00399 and W06108) are useful in the clinical assessment, diagnosis			
CC	and treatment of MS.			
SQ	Sequence 203 AA;			
<hr/>				
Query Match	66.1%; Score 113; DB 1; Length 203:			
Best Local Similarity	100.0%; Pred. No. 8.1e-104;			
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps				
OY	59 KDSHHPARTATYGSLPKSHGRTODENPVVHFENKITYTPRTPPSQSGRGSLSRFSWG 118			
DB	85 KDSHHPARTATYGSLPKSHGRTRDENVVHFENKITYTPRTPPSQSGKGGLSLSRFSWG 144			
OY	119 AEGORPGFGYGRASDYKSAAHGFKGYDAOGTLTKIRKLGGDRSSGSPMAR 171			
DB	145 AEGORPGFGYGRASDYKSAAHGFKGYDAOGTLTKIRKLGGDRSSGSPMAR 197			
<hr/>				
RESULT	7			
W06108	W06108 standard; Protein; 203 AA.			
AC	W06108;			
DT	01-FEB-1997 (first entry)			
DE	Foetal myelin basic protein MBP-X2Ser81/bact.			
KV	Myelin basic protein; MBP; MBP+X2Ser81; proteolipid protein; PLP;			
KW	multiple sclerosis; autoimmune disease; diagnosis; therapy;			
KM	T-lymphocyte; T-cell; anergy; apoptosis.			
OS	Synthetic.			
FH	Key	Location/Qualifiers		
FT	region	60..85	/label= X2	
FT		/note= "exon 2-encoded region, with Cys81ser		
FT	mutation"			
FT	peptide	198..203	/label= Hexa-histidine tag	
FT		/note= "the hexa-histidine tag facilitates		
FT		purification of the recombinant protein		
FT		from host cells"		
PN	W09634622-A1.			
PD	07-NOV-1996.			

PE 22-APR-1996: U05611.
 PR 02-MAY-1995: US-431648.
 PR 02-MAY-1995: US-431644.
 PR 07-JUN-1995: US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Mats L, McFarland HF, Mueller EE, Mueller JP,
 PI Nye SH, Pelfrey CM, Squinto SP, Watkins JA;
 PI WPI: 96-505898/50.
 DR N-PDSB: T41897.
 DR New human myelin basic protein and proteolipid protein variant(s)
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Disclosure: Page 82-83; 156pp: English.
 CC A 21.5 kDa foetal isoform (W06108) of myelin basic protein,
 CC MBP+X2SE81/Dacc., is the product of a DNA construct (T41897)
 CC based on the human foetal MBP+X2Cys81 isoform (W00399) but
 CC utilizing codons that are highly expressed in bacterial genes in
 CC place of the native codons (see also T41889) and incorporating a
 CC sequence coding for a hexa-histidine tail. This allows large-
 CC scale prodn. and purification of the MBP in bacterial hosts.
 CC Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) are
 CC useful in the clinical assessment, diagnosis and treatment of MS.
 SO Sequence 203 AA:

Query Match	66.1%;	Score 113;	DB 1;	Length 203;
Best Local Similarity	100.0%;	Pred. No. 8.1e-104;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy	59	KDSHHPATTAHGSJPPQKSHRTODENVYAEFFKNITYPRPPPSOGKRLSLSR	118
Db	85	KDSHHPATTAHGSJPPQKSHRTODENVYAEFFKNITYPRPPPSOGKRLSLSR	144
Oy	119	AEGQAPGCGYGRASDYKSAHKFGVDAGOSTLSKIFLGGDRSRS	171
Db	145	AEGQAPGCGYGRASDYKSAHKFGVDAGOSTLSKIFLGGDRSRS	197

RESULT	8
W06103	
ID	W06103 standard; Protein; 373 AA

DT	01-FEB-1997 (first entry)
DE	MP4 chimera (MBP21.5-delta PLP4 fusion).
KM	Proteolipid protein; PLP; delta PUP3; myelin basic protein; MBP;
KM	MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
KW	therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 Chimera.
OS	Synthetic.
PH	Key
FT	protein
FT	1.368 Location/Qualifiers
FT	/note="preferred protein of the invention"
FT	1.197
FT	/label= MBP21.5
FT	198. .200
FT	/label= Spacer
FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	210. .230
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	241. .261
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	242. .259
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	region
FT	1. .197
FT	/label= MBP21.5
FT	198. .200
FT	/label= Spacer
FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	210. .230
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	241. .261
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	242. .259
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	region
FT	1. .197
FT	/label= MBP21.5
FT	198. .200
FT	/label= Spacer
FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	210. .230
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	241. .261
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	242. .259
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	region
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FT	/label= MBP21.5
FT	198. .200
FT	/label= Spacer
FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
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FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	241. .261
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	242. .259
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	region
FT	1. .197
FT	/label= MBP21.5
FT	198. .200
FT	/label= Spacer
FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	210. .230
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	241. .261
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	242. .259
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	region
FT	1. .197
FT	/label= MBP21.5
FT	198. .200
FT	/label= Spacer
FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	210. .230
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	241. .261
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	242. .259
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
FT	region
FT	1. .197
FT	/label= MBP21.5
FT	198. .200
FT	/label= Spacer
FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"
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FT	/note="PLP epitope associated with MS"
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FT	/label= Epitope
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FT	/label= Epitope
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FT	/label= MBP21.5
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FT	201. .373
FT	/label= Delta_PLP4
FT	201. .205
FT	/note="synthetic N-terminal peptide not found in the native protein"
FT	208. .219
FT	/label= Epitope
FT	/note="PLP epitope associated with MS"</

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FT	region	213. . 234	/label= Epitope
FT		/note= "PUP epitope associated with MS"	
FT	region	256. . 269	/label= Epitope
FT		/note= "encephalitogenic epitope in mouse model"	
FT	region	292. . 304	/label= Epitope
FT		/note= "encephalitogenic epitope in mouse model"	
FT	peptide	369. . 373	/label= Epitope
FT		/note= "encephalitogenic epitope in mouse model"	
FT		/label= Histidine-tag	
FT		/note= "hexa-histidine tag facilitates recombinant protein purification"	
PM	W09634622-A1.		
PD	07-NOV-1996.		
PF	22-APR-1996; U05611.		
PR	02-MAY-1995; US-431648.		
PR	02-MAY-1995; US-431644.		
PR	07-JUN-1995; US-482114.		
PA	(ALEX-) ALEXION PHARM. INC.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PI	Lenardo KC, Malis L, Kocerand HF, Mueller EF, Mueller JP;		
PI	Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;		
DR	WPI; 96-505898/50.		
DR	N-PSDB; T41893.		
PT	New human myelin basic protein and proteolipid protein variant(s)		
PT	used in the assessment, diagnosis and treatment of multiple		
PT	sclerosis		
PS	Claim 34; Page 110-112; 156pp; English.		
CC	MP4 chimera (W06103) is a fusion protein composed of human myelin		
CC	basic protein (MBP) fetal isoform MBP21.5 (see also W00389) and		
CC	delta PLP4 (W06101), a proteolipid protein (PLP) mutein that lacks		
CC	all 4 hydrophobic domains of native human PLP (W06106) but		
CC	includes PLP epitopes associated with multiple sclerosis (MS). It		

Db 317 AEGQRFEGYGGASDYKSAHKGFKGVDAOGTISKIFKLGGRDSRGSPMARR 369

RESULT 10

ID W06102 standard; Protein: 385 AA.

AC W06102;

DT 01-FEB-1997 (first entry)

DE MP3 chimera (MBP21.5-delta PLP3 fusion).

KM Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

OS therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.

FT Key

FT domain

FT location/Qualifiers

FT 1..197

FT /label= MBP21.5

FT 198..200

FT /label= Spacer

FT 201..385

FT /label= Delta_PLP3

FT domain

FT W0634622-A1.

PN 07-NOV-1996.

PD 22-APR-1996: U05611.

PE 02-MAY-1995: US-431648.

PR 02-MAY-1995: US-431644.

PR 07-JUN-1995: US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Leonardo M.J. Matls L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Peifrey CM, Squinto SP, Wilkins JA.

DR WPI: 96-505898/50.

DR N-PSDB: T41892.

PT New human myelin basic protein and proteolipid protein variant(s) -

PT used in the assessment, diagnosis and treatment of multiple

PT sclerosis

PS Claim 33: Page 108-110; 156pp; English.

CC MP3 chimera (W06102) is a fusion protein composed of human myelin

CC basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and

CC delta PLP3 (W00400), a proteolipid protein (PLP) mutein that lacks

CC hydrophobic domains 1, 3 and 4 of native human PLP (W06106) but

CC includes PLP epitopes associated with multiple sclerosis (MS). It

CC can be expressed in E. coli transformants using a DNA construct

CC (T41892) contg. the MBP21.5-delta PLP3 gene fusion. MP3 chimera

CC and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)

CC are useful for the clinical assessment, diagnosis and treatment

CC of MS.

CC Sequence 385 AA:

SO

Query Match 66.1%; Score 113; DB 1; Length 385;

Best Local Similarity 100.0%; Pred. No. 1.4e-103;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 KDSHHARRAHYSLPQKSGRTQDENPVYHFKNTVTRTPPPSGKRGSLSRFSWG 118

DB 85 KDSHHARRAHYSLPQKSGRTQDENPVYHFKNTVTRTPPPSGKRGSLSRFSWG 144

OY 119 AEGQRFEGYGGASDYKSAHKGFKGVDAOGTISKIFKLGGRDSRGSPMARR 171

DB 145 AEGQRFEGYGGASDYKSAHKGFKGVDAOGTISKIFKLGGRDSRGSPMARR 197

RESULT 11

ID W06105

AC W06105 standard; Protein: 492 AA.

DT 01-FEB-1997 (first entry)

DE MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion).

KM Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

KW therapy; T-lymphocyte; T-cell; MMOGP4 chimera;

KW myelin oligodendrocyte glycoprotein; MOG.

FT Synthetic.

FT Key

FT protein

FT location/Qualifiers

FT 1..487

FT /note= "preferred protein of the invention"

FT 1..197

FT /label= MBP21.5

FT 198..319

FT /label= MOG

FT /note= "MOG extracellular domain"

FT 320..486

FT /label= Delta_PLP4

FT 327..338

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 329..349

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 360..380

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 361..278

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 363..376

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 367..378

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 375..388

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 376..388

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 387..400

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 389..402

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 411..423

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 411..426

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 414..425

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 433..445

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 445..456

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 445..458

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 470..484

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 332..353

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT 375..388

FT /label= Epitope

FT /note= "encephalitogenic epitope in mouse model"

FT 411..423

FT /label= Epitope

FT /note= "encephalitogenic epitope in mouse model"

FT 487..492

FT /label= Histidine_tag

FT /note= "hexa-histidine tag facilitates recombinant

FT W09634622-A1. protein purification"

PN 07-NOV-1996.

PD 22-APR-1996. U05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Leonardo MJ, Melis L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Pelletier CM, Squinto SP, Wilkins JA;

DR WPI; 96-505898/50.

DR N-PSDB: T41895.

PT New human myelin basic protein and proteolipid protein variant(s) -

PT used in the assessment, diagnosis and treatment of multiple

PT sclerosis

PS Claim 36; Page 115-117, 156pp; English.

CC MMOGP4 chimera (W06105) is a fusion protein composed of human myelin

CC basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the

CC extracellular domain of human myelin oligodendrocyte glycoprotein

CC (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutein.

CC MBP21.5, PLP and MOG are all recognised by autoreactive T cells from

CC multiple sclerosis (MS) patients. The chimera was produced using

CC a DNA construct (T41895) obtd. by inserting a sequence encoding the

CC MOG moiety into MP4 chimera DNA (see also T41893). MMOGP4 chimera

CC can be expressed in bacterial cell hosts. PLP and MBP polypeptides

CC (see also W00400, W06101-04, W06107-08) are useful in the clinical

CC assessment, diagnosis and treatment of MS.

SO Sequence 492 AA;

Query Match 66.1%; Score 113; DB 1; Length 492;

Best Local Similarity 100.0%; Pred. No. 1,7e-103;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KDSHHPARTATYAGSLPQKSHGRTOEDENPVHFFKNTVPRTPPPSGKGRGLSTRFSWG 118

DB 85 KDSHHPARTATYAGSLPQKSHGRTOEDENPVHFFKNTVPRTPPPSGKGRGLSTRFSWG 144

QY 119 AEGORPGFGYGRASDYKSAHKGFGVDAGTSLKIFRLGDRSGSPMAR 171

DB 145 AEGORPGFGYGRASDYKSAHKGFGVDAGTSLKIFRLGDRSGSPMAR 197

RESULT 12

ID R30736 standard; Protein; 170 AA.

AC R30736;

DT 21-MAY-1993 (first entry)

DE Human MBP.

KW Acetylcholine receptor; MHC; myelin basic protein; MBP.

OS Synthetic.

FH Key

FT modified_site 1 Location/Qualifiers

FT /note= "N-Ac-Ala"

FT modified_site 107

FT /note= "Me-Arg"

FT peptide 1..14

FT /note= "claim 30; page 68"

PN W09218150-A.

PD 29-OCT-1992.

PR 23-APR-1992; U03391.

PR 23-APR-1991; US-690640.

PA (ANER-) ANERGEN INC.

PI Clark BR, Lerch BL, Sharma SD;

DR WPI; 93-036056/04.

PT Pure major MHC-peptide complex - useful in treating deleterious

PT immune response such as autoimmunity.

PS Claim 30; Page 68 + Fig 7; 93pp; English.

CC A method is claimed for the prepn. of a pure major MHC-peptide

CC complex. The MHC component is a class II glycoprotein of the MHC

CC and the peptide comprises amino acids 1-14 of MBP.

SO Sequence 170 AA;

Query Match 53.8%; Score 92; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 3.3e-83;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 RTQDENPVHFFKNTVPRTPPPSGKGRGLSTRFSWGAEQORPGYGRASDYKSAH 139

DB 79 RTQDENPVHFFKNTVPRTPPPSGKGRGLSTRFSWGAEQORPGYGRASDYKSAH 138

QY 140 KGFKGVDAQGLSKIFRLGDRSGSPMAR 171

DB 139 KGFKGVDAQGLSKIFRLGDRSGSPMAR 170

RESULT 13

ID R35440 standard; Protein; 170 AA.

AC R35440;

DT 13-AUG-1993 (first entry)

DE Human basic myelin protein.

KW BMP; MS; multiple sclerosis; homologue; myelin basic protein; MBP.

OS Homo sapiens.

FH Key

FT peptide 61..106 Location/Qualifiers

FT /note= "neutralising fragment"

FT peptide 1..15

FT /note= "neutralising fragment"

FT peptide 4..18

FT /note= "neutralising fragment"

FT peptide 9..23

FT /note= "neutralising fragment"

FT peptide 15..35

FT /note= "neutralising fragment"

FT peptide 20..37

FT /note= "neutralising fragment"

FT peptide 31..46

FT /note= "neutralising fragment"

FT modified_site 1

FT /note= "acylated"

PN W09308212-A.

PD 29-APR-1993.

PR 15-OCT-1992; CA0448.

PR 22-OCT-1991; CA-053799.

PA (CAT2/) CAT2 I.

PA (MAR/) WARREN K G.

PI Catz I, Warren KG.

DR WPI; 93-152422/18.

PT Homologous peptide analogues of human basic myelin protein (BMP). Fragments

PT for treating multiple sclerosis

PS Disclosure; Fig 4; 26pp; English.

CC The sequence is that of human basic myelin protein (BMP). Fragments

CC of this sequence are claimed (see features) which are able to

CC neutralise anti-BMP antibodies and are thus useful in treatment of

CC multiple sclerosis. The fragments may be prepd. synthetically and

CC avoids the dangers associated with the use of the natural protein.

CC e.g. transmission of neuroviruses. Also the peptides are too small

CC to be immunogenic.

SO Sequence 170 AA;

Query Match 50.3%; Score 86; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 2.7e-77;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 PVVHFFKNTVPRTPPPSGKGRGLSTRFSWGAEQORPGYGRASDYKSAHKGFGV 145

DB 85 PVVHFFKNTVPRTPPPSGKGRGLSTRFSWGAEQORPGYGRASDYKSAHKGFGV 144

QY 146 DAQGLSKIFRLGDRSGSPMAR 171

DB 145 DAQGLSKIFRLGDRSGSPMAR 170

OM of: US-09-218-277-12 to: GenEmbl.* out_format : pfs

Date: Sep 26, 2000 8:02 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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Query length: 171

Database: GenEmbl.*

Database sequences: 972840

Database length: 89234806

Search time (sec): 762.360000

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Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_pr2:HUMRNAMBPF	+	922.00	1083.02	1781	L18866 Human Golli-mbp gene, c
gb_pr2:HUMMBPA	+	922.00	1081.72	2139	L13577 Human myelin basic prot
gb_pr3:HUM215MBP	+	899.00	1063.58	622	L41657 Homo sapiens synthetic m
gb_pr2:HUMMBPC	+	899.00	1058.54	1261	M30515 Human 21.5 KD myelin ba
gb_pr2:HUMMBP7K	+	847.50	998.74	1172	M30047 Human 17.3K myelin bas
gb_ro:RNO132897	+	836.00	991.20	510	AJ132897 Rattus norvegicus m
gb_pr2:HUMMBPB	+	824.50	971.45	1231	M30516 Human 20.2 KD myelin ba
gb_ro:RNO132898	+	813.00	963.24	588	AJ132898 Rattus norvegicus m
gb_ro:AF074337	+	724.50	861.48	450	AF074337 Cavia porcellus myelin
gb_ro:MUSMBP78M	+	716.50	841.70	1939	M15062 Mouse myelin basic prot
gb_ro:RATMBP2A	+	615.50	731.61	612	M25889 Rat myelin basic protein
gb_ro:RNO132895	+	611.50	730.19	387	AJ132895 Rattus norvegicus m
gb_ro:RATMBP	+	611.50	720.71	1464	K00512 rat myelin basic protei
gb_ov:GMBP	+	603.50	708.26	2256	X17103 Chicken mRNA for myelin
gb_ro:RNO132896	+	588.50	701.94	465	AJ132896 Rattus norvegicus m
gb_ro:MUSMBP72M	+	581.50	693.38	1990	M15060 Mouse myelin basic prot
gb_ro:MUSGOLLIA	+	540.00	633.17	2490	L07507 Mouse Golli-mbp mRNA, c
gb_ov:AB000736	+	505.50	601.43	738	AB000736 Xenopus laevis m
gb_pr2:HUMRNAMBPE	+	330.50	393.90	1054	L18865 Human Golli-mbp gene, c
gb_pr1:HSMBPX1	+	330.50	390.12	1791	X17286 H.sapiens MBP gene, ex
gb_pr2:HUMMBP1A	+	330.50	386.37	3031	M63599 Human myelin basic prot
gb_btgt1:AC021331	-	330.50	358.06	161183	AC021331 Homo sapiens clone
gb_btgt1:AP001810	+	330.50	337.99	162808	AP001810 Homo sapiens chrom
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gb_ro:MUSMBP1	+	294.00	358.78	361	M11291 Mouse myelin basic prote
gb_ro:MUSGOLLIB	+	294.00	349.09	1407	L07508 Mouse Golli-mbp mRNA, c
gb_ro:WMHMBPGR	+	294.00	340.54	4670	X67319 M.musculus mRNA for tra
gb_ro:MUSMBP1	+	284.00	350.99	208	L00398 Mouse 14kd, 17kd, 18.5kd
gb_ov:HMBPA	+	283.50	338.02	1183	X17664 H.francisci mRNA for my
gb_ov:REU44053	+	259.50	315.63	530	U44053 Raja erinacea myelin bas
gb_ov:SAU44052	+	257.50	313.29	246	U44052 Squalus acanthias myelin
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gb_btgt1:AP001649	+	220.50	227.72	0.0001	198597
gb_pr1:HSMBPX6	+	217.00	269.83	303	X17369 H.sapiens MBP gene, exon
gb_ov:AF010232	+	206.00	258.88	231	AF010232 Bos taurus myelin bas
gb_pr1:HSMBPX3	+	203.00	255.62	223	X17290 H.sapiens MBP gene, exon
gb_ro:MUSMBP5	+	196.50	249.41	183	M11532 Mouse myelin basic prote

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gb_ro:MUSMBPA6 + 195.50 249.75 8.2e-06 148 L00403 Mouse21.5kd myelin ba
gb_ro:MUSMBPA3 + 162.50 212.08 0.0010 129 L00400 Mouse 17kd and 21.5kd
gb_ro:MUSMBP2 + 158.50 204.94 0.0026 182 M11529 Mouse myelin basic pr
gb_ro:MUSMBPMLD2 + 148.50 192.55 0.0125 200 M36275 Mouse myelin basic pr

seq_name: gb_pr2:HUMRNAMBPF

seq_documentation_block:
LOCUS HUMRNAMBPF 1781 bp DNA PRI 08-MAR-1994
DEFINITION Human Golli-mbp gene, complete cds.
ACCESSION L18866
VERSION L18866.1 GI:435061
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1781)
Pribyl,T.M., Campagnoni,C.W., Kampf,K., Kashima,T., Handley,V.W.,
McMahon,J. and Campagnoni,A.T.
The human myelin basic protein gene is included within a
179-kilobase transcription unit: expression in the immune and
central nervous systems
PROC. Natl. Acad. Sci. U.S.A. 90 (22), 10695-10699 (1993)
FEATURES
Location/Qualifiers
1..1781
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/tissue_type="brain"
/map="18q22-qter"
1..176
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5'UTR
1..201
/evidence=experimental
177..252
/number=2
/evidence=experimental
202..1116
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/evidence=experimental
/db_xref="GI:435062"
/translation="MGNHAGKRELNAEKASTNSETNRGESEKRNELGELSRRTTSEDNE
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GELPRHRDGTILDSIGRFFGDRGAPKRGSKDSSHHPARTAHYGLSPQKSHGRTDEN
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253..340
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1117..>1781
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Ratio: 5.392 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-218-277-12 x HUMRNMBPF ..
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
651 CACAGCAAGTACCATGGACCATGCAGGATGGCTTCTCCCAAGGCACA 700
|||||
34 rGAspThrGlyLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
701 GAGACAGGGGATCTTGACTCCATCGGGCGCTCTTTGGCGGTGACAGG 750
|||||
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
|||||
751 GGTGGCCCAAGCGGGCTCTGGCAAGGACTCACACCACCGCGCAAGAAC 800
|||||
57 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
801 TGCTCACTATGGCTCCCTGCGCCAGAGATCACAGCGCGGACCAAGATG 850
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84 luAsnProValHisPhePheLysAsnIleValThrProArgThrPro 100
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851 AAAACCCCGTAGTCACCTCTCAAGAACATGTGACGCCCTCGCACACA 900
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101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
|||||
901 CCCCCTGCGCAGGAAGAGGGAGAGGACTGTCCCTGAGCAGATTAGCTG 950
|||||
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
|||||
951 GGGGGCCCAAGCCAGACAGACAGGATTTGGCTACGGAGCGAGCGTCCG 1000
|||||
134 spTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
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1001 ACTATAATCGCGTCACAGGGATTCAGGGAGTCGATGCCAGGGCAGC 1050
|||||
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
|||||
1051 CTTTCCAAAATTTTCAAGCTGGGAGGAGAGATAGTCGCTCTGGATCACC 1100
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167 oMetAlaArgArg 171
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1101 CATGGCTAGACGC 1113

seq_name: gb_pr2:HUMMBPA

seq_documentation_block:
LOCUS HUMMBPA 2139 bp mRNA PRI 07-JAN-1995
DEFINITION Human myelin basic protein (MBP) mRNA, complete cds.
ACCESSION M13577
VERSION M13577.1 GI:187408
KEYWORDS myelin basic protein.
SOURCE Human brain, mRNA to cDNA, clones pMBP-1 and pMBP-2.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2139)
AUTHORS Kamholz,J., de Ferra,F., Puckett,C. and Lazzarini,R.
TITLE Identification of three forms of human myelin basic protein by cDNA cloning
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)
MEDLINE 86259714
FEATURES
Location/Qualifiers
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/map="18q22-qter"
1..2139
/note="MBP mRNA"
37..552
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37..552
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FFGGDRGAPKRGSGKDSHPARTAHYGLSPKSHGRTODENPVVHFKNIVTPPTPP
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DSRSGSPVARR"
BASE COUNT 519 a 619 c 556 g 445 t
ORIGIN Chromosome 18q22-qter; 1212 bp upstream of EcoRI site.

alignment_scores:
Quality: 922.00 Length: 171
Ratio: 5.392 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x HUMMBPA ..
Align seg 1/1 to: HUMMBPA from: 1 to: 2139

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|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
87 CACAGCAAGTACCATGGACCATGCAGGATGGCTTCTCCCAAGGCACA 136
|||||
34 rGAspThrGlyLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
137 GAGACAGGGGATCTTGACTCCATCGGGCGCTCTTTGGCGGTGACAGG 186
|||||
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
|||||
187 GGTGGCCCAAGCGGGCTCTGGCAAGGACTCACACCACCGCGCAAGAAC 236
|||||
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
237 TGCTCACTATGGCTCCCTGCGCCAGAGATCACAGCGCGGACCAAGATG 286
|||||
84 luAsnProValHisPhePheLysAsnIleValThrProArgThrPro 100
|||||
287 AAAACCCCGTAGTCACCTCTCAAGAACATGTGACGCCCTCGCACACA 336
|||||
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
|||||
337 CCCCCTGCGCAGGAAGAGGGAGAGGACTGTCCCTGAGCAGATTAGCTG 386
|||||
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
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387 GGGGGCCGAAGCCAGACACGAGGATTTGGCTACGAGGCGAGAGCGTCGC 436
134 sPTyLysSerAlaHisLysGlyPheLysGlyValaspAlaGlnGlyThr 150
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437 ACTATAATCGGCTCACAGGAGATTCAAGGGAGTCGATGCCAGGGCAGC 486
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
|||||
487 CTTTCCAAATTTTAACTGGGAGGAGAGATAGTCGCTCGGATCACC 536
167 oMetalaArgArg 171
|||||
537 CATGGCTAGACGC 549
seq_name: gb_pr3:HUM215MBP

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seq_documentation_block: 622 bp DNA PRI 20-JAN-1996
LOCUS HUM215MBP
DEFINITION Homo sapiens synthetic myelin basic protein 21.5 kDa isoform gene,
complete cds.
ACCESSION L41657
VERSION L41657.1 GI:1162921
KEYWORDS myelin basic protein; synthetic DNA; synthetic gene.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Kamholz,J., de Ferra,F., Puckett,C. and Lazzarini,R.
TITLE Identification of three forms of human myelin basic protein by cDNA
Cloning
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)
MEDLINE 86259714
REFERENCE 2 (bases 1 to 622)
AUTHORS Nye,S.H., Pelfrey,C.M., Burkwit,J.J., Voskuhl,R.R., Lenardo,M.J.
and Mueller,J.P.
TITLE Purification of immunologically active recombinant 21.5 kDa isoform
of human myelin basic protein
JOURNAL Mol. Immunol. 32 (14-15), 1131-1141 (1995)
MEDLINE 96128281
COMMENT Sequence M13577 overlaps this sequence.
FEATURES
Location/Qualifiers
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1..622
1..622
4..615
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4..615
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/product="myelin basic protein"
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BASE COUNT 120 a 220 c 167 g 115 t
ORIGIN

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Quality: 899.00 Length: 197
Ratio: 5.257 Gaps: 1
Percent Similarity: 86.802 Percent Identity: 86.802
alignment_block:
source
1..1261

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US-09-218-277-12 x HUM215MBP
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
54 CACGCCAGCACCATGGACCATGCCGTCATGGCTTCCTCGCGGTCCACC 103
34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
|||||
104 GTGACACCGGCATCCTGGACTCCATCGCCGCTTCTTCGGCGGTGACCGT 153
51 GlyAlaProLysArgGlySerGly..... 58
|||||
154 GGTGGCGCGAAACGTCGTCTGGCAAGTGCCTGGCTGAAACCGGGCGC 203
58 ..... 58
204 TAGCCCGCTGCCGTCTCATGCCGTAGCCAGCGGGCCTGTGCACATGT 253
59 ..LysAspSerHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
254 ACAAGACTCCACACCCCGGCTGTACCGGCACACTATGGCTCCCTGCCG 303
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
|||||
304 CAGAAATCCAGCGCGTACCCAGGATGAAACCCGGTGGTGCACTTCTT 353
91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
|||||
354 CAAAACATTTGACCCCGCTAGCCCGCCGCTCTCAGGCAAAAGGCC 403
108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
|||||
404 GTGGCCTGTCCCTGAGCCGTTTCAGCTGGGCGCGGAAGCGCAGCGTCG 453
125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysGln 141
|||||
454 GGTCTCGGCTACGGGGCGCGTGGTCCGACTATAAATCTGTCAAAAGG 503
141 yPheLysGlyValaspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
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504 CTTCAAAGCGGTGGATGCCAGGCAACCTGTCCAAAATTTTCAAACCTGG 553
158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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554 GCGGCGGTGATAGCGGTTCTGGCTCTCCGATGGCTAGACGT 594

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seq_name: gb_pr2:HUMMBPC

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seq_documentation_block: 1261 bp mRNA PRI 07-JAN-1995
LOCUS HUMMBPC
DEFINITION Human 21.5 kD myelin basic protein (RK41) mRNA, complete cds.
ACCESSION M30515
VERSION M30515.1 GI:187412
KEYWORDS alternative splicing; myelin basic protein.
SOURCE Human spinal cord, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1261)
AUTHORS Roth,H.J., Kronquist,K.E., Kerlero de Rosbo,N., Crandall,B.F. and
Campagnoni,A.I.
TITLE Evidence for the expression of four myelin basic protein variants
in the developing human spinal cord through cDNA cloning
JOURNAL J. Neurosci. Res. 17 (4), 321-328 (1987)
MEDLINE 87311781
FEATURES Location/Qualifiers
source
1..1261

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/protein_id="AA59564.1"
/db_xref="GI:307162"
/translation="MASQKRPQSHGSKYLATASTMDHARHGFLEPRHRTGILDSIGR
FFGDRGAPKRGSKVPLKGRPLPSHARSQPLCNMYKDSHPHARTAHYGLSPQK
SHGTODENPVVHFKNIVTPTPPPSQKGRGLSLSRFSWGAEGQRPFGYGGGRAD
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BASE COUNT 288 a 378 c 336 g 259 t
ORIGIN

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  Quality: 899.00      Length: 197
  Ratio: 5.257        Gaps: 1
Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:
US-09-218-277-12 x HUMMBPC ..
Align seg 1/1 to: HUMMBPC from: 1 to: 1261

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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHis 34
|||||
58 CACAGCAAGTACCATGGACCATCCAGGCAATGCTTCTCTCCCAAGGACA 107
|||||
34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
|||||
108 GAGACACGGGCATCTTGACTCCATCGGGCGCTCTTTGGCGGTGACAGG 157
|||||
51 GlyAlaProLysArgGlySerGly..... 58
|||||
158 GGTGCGCCCAAGCGGGGCTCTGGCAAGGTACCTGGCTAAAGCGGCGCG 207
|||||
58 ..... 58
208 GAGCCCTCTCCCTCTCATGCGCGCAGCCAGCTGGCTGTGCAACATGT 257
|||||
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
258 ACAAGGACTCACACCACCGCGCAAGAACTGCTCCTATGCTCCCTGCC 307
|||||
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
|||||
308 CAGAAGTACACCGCGCGGACCCCAAGATGAACACCCCGTAGCTCCTTT 357
|||||
91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGly 108
|||||
358 CAAGAACATTTGTACGCTCGCACACACCCCGTGCAGGGAAGGGA 407
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108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
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408 GAGGACTGTCCCTGAGCAGATTTAGCTGGGGCGCGGAAGCCAGACCA 457
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125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLys 141
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458 GGATTGGCTACGAGGACGAGCGTCCGACTATAAATCGGCTCACAAGG 507
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141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
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508 ATTCAGGGAGTGCATGCCCGAGGCGCGCTTTCAAAATTTTCAAGCTGG 557

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158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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seq_name: gb_pr2:HUMMBP17K

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seq_documentation_block:
LOCUS HUMMBP17K 1172 bp mRNA PRI 07-JAN-1995
DEFINITION Human 17.3K myelin basic protein (MBP) mRNA, complete cds.
ACCESSION M30047
VERSION M30047.1 GI:187400
KEYWORDS myelin basic protein.
SOURCE Human fetal spinal cord, cDNA to mRNA, clone KK36.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1172)
AUTHORS Roth,H.J., Kronquist,K., Pretorius,P.J., Crandall,B.F. and
Campagnoni,A.T.
TITLE Isolation and characterization of a cDNA coding for a novel human
JOURNAL 17.3K myelin basic protein (MBP) variant
MEDLINE J. Neurosci. Res. 16 (1), 227-238 (1986)
FEATURES
86308101 Location/Qualifiers
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/protein_id="AA59564.1"
/db_xref="GI:307162"
/translation="MASQKRPQSHGSKYLATASTMDHARHGFLEPRHRTGILDSIGR
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BASE COUNT 273 a 353 c 306 g 240 t
ORIGIN

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  Ratio: 5.297        Gaps: 1
Percent Similarity: 93.567 Percent Identity: 93.567

alignment_block:
US-09-218-277-12 x HUMMBP17K ..
Align seg 1/1 to: HUMMBP17K from: 1 to: 1172
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHis 34
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83 CACAGCAAGTACCATGGACCATCCAGGCAATGCTTCTCTCCCAAGGACA 132
|||||
34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
|||||
133 GAGACACGGGCATCTTGACTCCATCGGGCGCTTCTTTGGCGGTGACAG 182
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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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183 GGTGCGCCCAAGCGGGGCTCTGGCAAGGACTCACACCACCGCGCAAGAC 232
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67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84

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233 TGCTCACTACGCTCCCTGCCCCAGAGTCACACGGCGGACCAAGATG 282
84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
283 AAAACCCCGTAGCTCCACATCTTTCAAGAACATTTGTACGCTCGCACACCA 332
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
333 CCCCCGTGCAGGGAAG..... 350
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrglyGlyArgAlaSerA 134
351 .GGGCGCGAAGCCAGACACCAAGATTGGCTACGGAGCAGAGCGTCCG 399
134 sPTyLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
400 ACTATAAATCGGCTCACAGGGATTCAAGGGAGTCGATGCCAGGGCAGC 449
151 LeuSerLysIlePheLysLeuGlyArgAspSerArgSerGlySerPr 167
450 CTTTCCAAATTTTAAGCTGGAGAGAGATAGTCGCTCTGGATCACC 499
167 oMetAlaArgArg 171
500 CATGGCTAGACGC 512

seq_name: gb_ro:RN0132897

seq_documentation_block:
LOCUS RN0132897 510 bp mRNA ROD 11-FEB-1999
DEFINITION Rattus norvegicus mRNA for myelin basic protein, 18.5 kDa isoform.
ACCESSION AJ132897
VERSION AJ132897.1 GI:4454314
KEYWORDS isoform; mbp gene; myelin; myelin basic protein.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
AUTHORS Lobell,A.M.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
SWEDEN
REFERENCE
AUTHORS Lobell,A.M. and Wigzell,H.
JOURNAL Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
SWEDEN
FEATURES
Source
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/protein_id="CAA10806.1"
/db_xref="GI:4454315"
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BASE COUNT 134 a 155 c 139 g 82 t
ORIGIN

alignment_scores:
Quality: 836.00 Length: 172
Ratio: 4.976 Gaps: 3

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Percent Similarity: 97.674 Percent Identity: 93.605
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US-09-218-277-12 x RN0132897 ..
Align seg 1/1 to: RN0132897 from: 1 to: 510

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|||||
51 CACAGCAAGTACCATTGGACCATGCCCGCATGGCTTCCTCCCAAGGCACA 100
34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
101 GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTAGGGGTGACAG 150
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
|||||
151 GGTGGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC.....ACAAGAAC 194
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
195 TACCACACTACGGCTCCCTGCCCCAGAGATCGCAG...AGGACCCAGATG 241
84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
|||||
242 AAAACCCAGTAGTACACTTCTTCAAGAACATTGTGACACCTCGTACACCC 291
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
|||||
292 CTTCCATCCCAAGGAAGGAGAGGCGCTGCTCCCTCAGCAGATTAGTGTG 341
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrglyGlyArgAlaSerA 134
|||||
342 GGGGCGCCAGGGCGAGAGCCAGGATTTGGCTACGGAGCAGAGCTTCGG 391
134 sPTyLysSerAlaHisLysGlyPheLysGlyVal...AspAlaGlnGly 149
|||||
392 ACTATAAATCGGCTCACAGGGATTCAAGGGGCGCTACGAGCAGCCAGGC 441
150 ThrLeuSerLysIlePheLysLeuGlyArgAspSerArgSerGlySe 166
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442 ACGCTTCCAAATCTTTAAGCTGGAGAGAGAGACAGCCGCTGTGATC 491
166 rProMetAlaArgArg 171
|||||
492 TCCCATAGCAGACGC 507

seq_name: gb_pr2:HUMMBPB

seq_documentation_block:
LOCUS HUMMBPB 1231 bp mRNA PRI 07-JAN-1995
DEFINITION Human 20.2 kD myelin basic protein (RK187) mRNA, complete cds.
ACCESSION M30516
VERSION M30516.1 GI:187410
KEYWORDS alternative splicing; myelin basic protein.
SOURCE Human spinal cord, CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Roth,H.J., Kronquist,K.E., Kerlero de Rosbo,N., Crandall,B.F. and
Campagnoni,A.T.
TITLE Evidence for the expression of four myelin basic protein variants
in the developing human spinal cord through cDNA cloning
JOURNAL J. Neurosci. Res. 17 (4), 321-328 (1987)
MEDLINE 87311781
FEATURES
Location/Qualifiers
source
1..1231
/organism="Homo sapiens"

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CDS
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/note="myelin basic protein"
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/db_xref="DB:G00-119-379"
/protein_id="AA059563.1"
/db_xref="GI:307161"
/translation="WASOKRPSORHGSKYLATAMDHARGFLPRHRTGTGILDSIGR
FEGDRGAPKRGSGKVPWLKPSRPLSHARSPLCHMYKDSHPARTAHVGSIPQK
SGRGTQDENPVVHFKNIVTPPTPPSQGKRGGLSLRFSWGAESQKPGFGYGRASDYKS
DAQGLSKIFLGGDRSDSGSPMAR"
BASE COUNT 281 a 374 c 323 g 253 t
ORIGIN

alignment_scores:
  Quality: 824.50      Length: 197
  Ratio: 5.153        Gaps: 2
  Percent Similarity: 81.218      Percent Identity: 81.218

alignment_block:
US-09-218-277-12 x HUMMBPB ..
Align seg 1/1 to: HUMMBPB from: 1 to: 1231

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
11 ATGGCGTCACAGAAGAGACCCCTCCAGAGCAGGATCCCAAGTACCTGGC 60
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
61 CACAGCAAGTACCATGACCATGCCAGCATGGCTTCTCCCAAGGCACA 110
|||||
34 rGAspThrGlyLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
111 GAGACAGGGCATCTTGACTCCATCCATCGGGCGCTTCTTTGGCGGTGACAGG 160
|||||
51 GlyAlaProLysArgGlySerGly..... 58
161 GGTGCGCCCAAGCGGGCTCTGGCAAGGTACCTGGCTAAAGCGGGCGG 210
|||||
58 ..... 58
211 GAGCCCTCTGCCCTCTCATGCCCGCAGCCAGCCTGGGCTGTGCAACATGT 260
|||||
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
261 ACAAGGACTCACACACCGCGCAAGAACTGCTACACGGCTCCCTGCC 310
|||||
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
|||||
*311 CAGAAGTCACACGCGCGGACCAAGATGAACCCCGTAGTCCACTCTT 360
|||||
91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
|||||
361 CAAGAACAATTGTGACGCTCCACACACACCCCGCTCGCAGGGAAG.... 406
|||||
108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
|||||
407 .....GGGGCCGAAGGCCAGAGACCA 427
|||||
125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
|||||
428 GCATTGGCTACGAGGCGAGCGCTCCGACTATTAATCGGCTCAAGGG 477
|||||
141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
|||||
478 ATTCAGGGAGTCGATGCCAGGCGCACGCTTCCAAAAATTTTAAAGCTGG 527
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158 lyGlyArgaspSerArgSerGlySerProMetAlaArgArg 171
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528 GAGGAAGAGATAGTCGCTCTGGATCACCCTAGCTAGACGC 568

seq_name: gb_ro:RNO132898

seq_documentation_block:
LOCUS RNO132898 588 bp mRNA ROD 18-FEB-2000
DEFINITION Rattus norvegicus mRNA for myelin basic protein, 21.5 kDa isoform.
ACCESSION AJ132898
VERSION AJ132898.1 GI:4454316
KEYWORDS isoform; mbp gene; myelin; myelin basic protein.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 588)
AUTHORS Weissert,R., Lobell,A.M., de Graaf,K.L., Eltayeb,S.Y.,
Andersson,R., Olszen,T. and Wigzell,H.
TITLE Protective DNA vaccination against organ-specific autoimmunity is
highly specific and discriminates between single amino acid
substitutions in the peptide autoantigen
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97, 166-1694 (2000)
REFERENCE 2 (bases 1 to 588)
AUTHORS Lobell,A.M.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
SWEDEN

FEATURES
source
1..588
/organism="Rattus norvegicus"
/strain="Lewis rat"
/db_xref="taxon:10116"
1..588
/gene="mbp"
1..588
/gene="mbp"
/codon_start=1
/product="myelin basic protein"
/protein_id="CAA10807.1"
/db_xref="GI:4454317"
/db_xref="SPTREMBL:Q92134"
/translation="MASQKRPSSORHGSKYLATAMDHARGFLPRHRTGTGILDSIGR
FFSGDRGAPKRGSGKVPWLKPSRPLSHARSPLCHMYKDSHTRTTHYGLSPKSKO
RTODENPVVHFKNIVTPPTPPSQGKRGGLSLRFSWGAESQKPGFGYGRASDYKS
AHKGFKAYDAQGLSKIFLGGDRSDSGSPMAR"
BASE COUNT 148 a 184 c 160 g 96 t
ORIGIN

alignment_scores:
  Quality: 813.00      Length: 198
  Ratio: 4.839        Gaps: 4
  Percent Similarity: 84.848      Percent Identity: 81.313

alignment_block:
US-09-218-277-12 x RNO132898 ..
Align seg 1/1 to: RNO132898 from: 1 to: 588

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
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1 ATGGCATCACAAGAAGAGACCCCTCACAGCGACACGATCCCAAGTACTGGC 50
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51 CACAGCAAGTACCATGACCATGCCCGGCGATGGCTTCTCCCAAGGCACA 100
|||||
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
101 GAGACAGGCGATCCTTGACTCCATCGGGCGCTTCTTTAGCGGTGACAGG 150
|||||

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51 GlyAlaProLysArgGlySerGly..... 58
|||||
151 GGTGCCCCCAAGCGGGCTCTGCAAGGTACCTTGCTTAAGCAGAGCGG 200
58 ..... 58
201 GAGCCCTCTGCCTTCATCGCCGCGAGCGCTCCCGGCTGTGCCACATGT 250
59 ..LysAspSerHisHisProAlaAraThrAlaHisTyrGlySerLeuPro 74
|||||
251 ACAAGGACTCACAC.....ACAAGAACTACCCACTACGGCTCCCTGCC 294
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePhe 91
|||||
295 CAGAACTCCGAG...AGGACCCAGATGAACCCAGTAGTCCACTTC 341
91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
342 CAAGAACATTGTGACACCTCGTACACCCCTCCATCCCAAGGAAGGGA 391
108 rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
|||||
392 GAGGCGTGTCCTACAGATTAGCTGGGGCGCGAGGGCGCAGAGCCA 441
125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
|||||
442 GGAATTTGGCTACGAGGCGAGCTCCGACTATAAATCGCTCACAA 491
141 yPheLysGlyVal...AspAlaGlnGlyThrLeuSerLysIlePheLys 157
|||||
492 ATTCAAGGGGCTACGACGCCCGAGGCGCTTTCCAAATCTTTAAGC 541
157 euGlyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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542 TGGGAGGAAGACAGACCGCTCTGGATCTCCCATAGCAAGAGCG 585
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seq_name: gb_ro:AF074337

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seq_documentation_block:
LOCUS AF074337 450 bp mRNA ROD 14-JUL-1998
DEFINITION Cavia porcellus myelin basic protein (MBP) mRNA, partial cds.
ACCESSION AF074337
VERSION AF074337.1 GI:3309628
KEYWORDS domestic guinea pig.
SOURCE Cavia porcellus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
  Kim,G., Tanuma,N. and Matsumoto,Y.
  1 (bases 1 to 450)
  DNA vaccination using Guinea pig myelin basic protein coding region
  in experimental autoimmune encephalomyelitis
  Unpublished
  2 (bases 1 to 450)
  Kim,G., Tanuma,N. and Matsumoto,Y.
  Direct Submission
  Submitted (24-JUN-1998) Neuropathology, Tokyo Metropolitan
  Institute for Neuroscience, Musashidai 2-6, Fuchu, Tokyo 183-8526,
  Japan
FEATURES
  source Location/Qualifiers
    1..450
      /organism="Cavia porcellus"
      /strain="Hartley"
      /db_xref="taxon:10141"
      /tissue_type="spinal cord"
      <1..>450
      /gene="MBP"
      <1..>450
      /gene="MBP"
      /codon_start=1
      /product="myelin basic protein"
      /protein_id="AAC36130.1"
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/db_xref="GI:3309628"
/translation="SQRHGSKYLATATMDHARHGLPRHRDTGILDISGRFSGSDRA
APRSGKSDHSHARTHYGLSKQSQRSDENPVHFFNIVTPRPPPSQKGRGL
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BASE COUNT 119 a 134 c 122 g 75 t
ORIGIN
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alignment_scores:
  Quality: 724.50 Length: 154
  Ratio: 4.895 Gaps: 4
  Percent Similarity: 96.104 Percent Identity: 91.558
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alignment_block:

US-09-218-277-12 x AF074337 ..

Align seg 1/1 to: AF074337 from: 1 to: 450

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8 SerGlnArgHisGlySerLysTyrLeuAlaThrAlaSerThrMetAspH1 24
|||||
1 TCCAGAGGCACGGATCCAGTACCTGGCCACAGCAAGTACCATTGACCA 50
24 salaargHisGlyPheLeuProArgHisargAspThrGlyIleLeuAsp 41
|||||
51 TCCAGGCATGGCTTCTCCCAAGGCACAGACACAGCATCCTTGACT 100
41 erIleGlyArgPhePheGlyGlyAspArgGlyAlaProLysArgGlySer 57
|||||
101 CCATCGGGCGCTTCTTGGCAGTGACAGGGCTGCGCCCAAGCGGGCTCC 150
58 GlyLysAspSerHisHisProAlaargThrAlaHisTyrGlySerLeuPr 74
|||||
151 GGCAGGAGCTCACATCAGCAGCAAGAACGCCACTATGGCTCCCTGCC 200
74 OGlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPheP 91
|||||
201 CCAGAACTCGCAG...CGTCCCAAGATGAACCCCTGTAGTCCACTTCT 247
91 heLysAsnIleValThrProArgThrProProSerGlnGlyLysGly 107
|||||
248 TCAAGAACAATTGTGACACCCCGCACACCTCTCCGTCTCAAGGAAGGGA 297
108 ArgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPr 124
|||||
298 AGAGGATTGTCCTCAGCAGATTTAGCTGGGAGCGCGAGGGCAGAAACC 347
124 OGlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
|||||
348 AGGATTGGCTATGAGGCGAGAGCT...GACTACAAATCC.....AAG 388
141 lyPheLysGlyVal...AspAlaGlnGlyThrLeuSerLysIlePheLys 156
|||||
389 GATTCAAGGGGCGCCATGATGCCAGGGCAGCGCTTTCCAAATCTTTAAA 438
157 LeuGlyGlyArg 160
|||||
439 CTGGGAGGAAGA 450
seq_name: gb_ro:MUSMBP78M
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seq_documentation_block:
LOCUS MUSMBP78M 1939 bp mRNA ROD 15-AUG-1995
DEFINITION Mouse myelin basic protein mRNA, 3' end, clone NK-M78.
ACCESSION M15062
VERSION M15062.1 GI:199050
KEYWORDS alternative splicing; myelin basic protein.
SOURCE Mus musculus (strain C57BL/6J, sub-species domesticus) (clone:
NK-M78.) 18-day-old brain cDNA to mRNA.
ORGANISM Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 1939)
  Newmann,S., Kitamura,K. and Campagnoni,A.T.
```

TITLE Identification of a cDNA coding for a fifth form of myelin basic protein in mouse

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (3), 886-890 (1987)

MEDLINE 87118269

COMMENT Draft entry and computer-readable sequence for [1] kindly provided by A.T. Campagnoni, 30-MAR-1987.

As many as eight myelin basic proteins can be encoded by the same gene by alternative splicing. The sequence below is missing exons 2 and 5 of the gene and encodes a 17.22 kDa myelin basic protein. The variations in the 3' untranslated regions between the two clones may be reverse transcriptase errors [1].

FEATURES**source**

1..1939
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /sub_species="domesticus"
 /db_xref="taxon:10090"
 /clone="NK-M78"
 /dev_stage="18-day-old"
 /tissue_type="brain"
 <1..452
 /note="myelin basic protein"

CDS

/codon_start=3
 /protein_id="AA059712.1"
 /db_xref="GI:190051"
 /translation="RSKYLATASTMDHARHGFLEPRHDTGILDSIGRFFSGDRGAPKR
 GSKDSHTTHYSUPQSGHRTQDENPVVHFKNITVPTPTPPSQGKAGQKPG
 FGVGGRASDYKSAHKFGKAYDAQGTLSKIFKLGDRDSRSGSPMARR"
 1023
 /note="t in M78; c in M72"
 /replace="c"
 1700
 /note="t in M78; c in M72"
 /replace="c"

BASE COUNT 447 a 545 c 517 g 428 t 2 others

ORIGIN 35 bp upstream of Avasi site.

alignment_scores:
 Quality: 716.50 Length: 161
 Ratio: 4.908 Gaps: 4
 Percent Similarity: 90.683 Percent Identity: 87.578

alignment_block:
 US-09-218-277-12 x MUSMBP78M ..

Align seg 1/1 to: MUSMBP78M from: 1 to: 1939

13 SerLysTyrLeuAlaThrAlaSerThrMetAspHisAlaArgHisGlyPhe 29
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 6 TCCAGTAGCTGGCCACAGCAAGTACCATGGACCATGCCAGGCATGGCTT 55
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 29 eLeuProArgHisArgAspThrGlyIleLeuAspSerIleGlyArgPheP 46
 |||||
 56 CCTCCAGGACAGACAGACGGGCATCTTGACTCCATCGGGCGCTTCT 105
 |||||
 46 heGlyGlyAspArgGlyAlaProLysArgGlySerGlyLysAspSerHis 62
 |||||
 106 TTAGCGGTGACAGGGGTGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC 155
 |||||
 63 HisProAlaArgThrAlaHisTyrGlySerLeuProGlnLysSer...H1 78
 :::::ACGGAAGTACCATATATGGCTCCCTGCCCAAGAGTCCGACGA 199
 |||||
 78 sGlyArgThrGlnAspGluAsnProValValHisPhePheLysAsnIleV 95
 |||||
 200 CGCGCGGACCCAGATGAARACCCAGTAGTCCATTCTTCAAGACATG 249
 |||||
 95 alThrProArgThrProProSerGlnGlyLysGlyArgGlyLeuSer 111
 |||||
 250 TGACACCTCGAACACCACTCCATCCCAAGGAAG..... 284
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 112 LeuSerArgPheSerTrpGlyAlaGluGlyGlnArgProGlyPheGlyTy 128
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285GGGGCCGAGGGCAGAGCCAGGATTGGCTA 316
 |||||
 128 rGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGlyPheLysGlyV 145
 |||||
 317 CGGAGGCGAGAGCTTCGACTATAATCGGCTCACAGGGATTCAAGGGG 366
 |||||
 145 al....AspAlaGlnGlyThrLeuSerLysLysPheLysLeuGlyArg 160
 ::|||
 367 CCTACGACGCCAGGGCAGCTTCCAAATCTTTAAGCTGGGAGGAAGA 416
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 161 AspSerArgSerGlySerProMetAlaArgArg 171
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 417 GACAGCGCTCTGGATCTCCATGGCGAGACGC 449
 |||||

seq_name: gb_ro:RATMBP2A

seq_documentation_block: 612 bp mRNA ROD 27-APR-1993

LOCUS RATMBP2A
DEFINITION Rat myelin basic protein mRNA, complete cds.
ACCESSION M25889
VERSION M25889.1 GI:205321

KEYWORDS myelin basic protein.
SOURCE Rat (18-day old) brain, cDNA to mRNA, clone pMBP2.
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 612)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

AUTHORS Schaich,M., Budzinski,R.-M. and Stoffel,W.

TITLE Cloned proteolipid protein and myelin basic pritein cDNA:
 Transcription of the two genes during myelination

JOURNAL Biol. Chem. Hoppe-Seyler 367, 825-834 (1986)
MEDLINE 87026249
FEATURES

source

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 /db_xref="GI:205322"

CDS

/translation="MASQRFSQRHGSKYLATASTMDHARHGFLEPRHDTGILDSIGR
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 151 a 195 c 148 g 118 t

BASE COUNT 151 a 195 c 148 g 118 t

ORIGIN

alignment_scores:

Quality: 615.50 Length: 171
 Ratio: 4.809 Gaps: 3
 Percent Similarity: 74.854 Percent Identity: 72.515

alignment_block:

US-09-218-277-12 x RATMBP2A ..

Align seg 1/1 to: RATMBP2A from: 1 to: 612

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 41 ATGGCATCACAGAGAGACCTCACAGCAGACGGATCCCAAGTACTTGGC 90
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 17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHis 34
 |||||
 91 CACAGCAAGTACCATGGACCATGCCCGGCATGGCTCTCTCCCAAGGCACA 140
 |||||
 34 rGaspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
 |||||
 141 GAGACAGCGGCATCTTGACTCCATCGGGCGCTCTTTAGCGGTGACAGG 190
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 51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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191 GGTGGCCCAAGCGGGCTCTGGCAAGGACTCACAC.....ACAAGAAC 234
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
235 TACCCACATACGCTCCCTGCCCAAGTCCGAG...AGGACCCCAAGATG 281
84 luAsnProValIleHisPhePheLysAsnIleValThrProArgThrPro 100
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
282 AAAACCCAGTAGTCCATCTTCAGACACATGTGACACCTCGTACACCC 331
101 ProProSerGlnGlySerGlyArgGlyLeuSerLeuSerArgPheSerTr 117
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
332 CCTCCATCCCAAGGAAGGGAGAGCGCTGTCCTCCAGCAGATTTAGCTG 381
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSerA 134
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
382 G..... 382
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
382 ..... 382
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
383 ..... 411
167 oMetAlaArgArg 171
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412 CATGGCAAGACGC 424

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seq_name: gb_ro:RN0132895

seq_documentation_block:

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LOCUS      RN0132895      387 bp      mRNA      ROD      11-FEB-1999
DEFINITION Rattus norvegicus mRNA for myelin basic protein, 14kDa isoform.
ACCESSION  AJ132895
VERSION    AJ132895.1 GI:4454310
KEYWORDS   isoform; mbp gene; myelin; myelin basic protein.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

```

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REFERENCE  1 (bases 1 to 387)
AUTHORS   Lobell,A.M.
TITLE     Direct Submission
JOURNAL   Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
          Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
          SWEDEN

```

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REFERENCE  2 (bases 1 to 387)
AUTHORS   Lobell,A.M. and Wigzell,H.
JOURNAL   Unpublished
FEATURES   Location/Qualifiers
            source          1..387
                        /organism="Rattus norvegicus"
                        /strain="Lewis rat"
                        /db_xref="taxon:10116"

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gene 1..387

CDS 1..387

1..387

/gene="mbp"

/note="14kDa isoform"

/codon_start=1

/product="myelin basic protein"

/protein_id="CAA10804.1"

/db_xref="GI:4454311"

/translation="MASQKRPQRHSGSKYLATSTMDHARGFLPRHRDGIIDSTGR

FFSGDGPAGRGSKSHSTHTYGLSPQRSQTDENPVVHEFKNIYVTRTPPSQG

KGGLSLSRFSWGRDRSGSPARR"

BASE COUNT 103 a 124 c 99 g 61 t

ORIGIN

alignment_scores:

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Quality: 611.50      Length: 171
Ratio: 4.777      Gaps: 3
Percent Similarity: 74.854      Percent Identity: 71.930
alignment_block:
US-09-218-277-12 x RN0132895 ..
Align seg 1/1 to: RN0132895 from: 1 to: 387
1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1 ATGCATCACAGAAGAGACCCCTCACAGCGACAGCATCCAAAGTACTTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
51 CACAGCAAGTACCATGGACCATGCCGCGCTCTCTCCCAAGGCACA 100
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
101 GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTAGCGGTGACAG 150
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
151 GGTGGCCCAAGCGGGCTCTGGCAAGGACTCACAC.....ACAAGAAC 194
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
195 TACCCACTACGCTCCCTGCCCAAGTCCGAG...AGGACCCCAAGATG 241
84 luAsnProValIleHisPheLysAsnIleValThrProArgThrPro 100
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
242 AAAACCCAGTAGTCCATCTTCAGACACATGTGACACCTCGTACACCC 291
101 ProProSerGlnGlySerGlyArgGlyLeuSerLeuSerArgPheSerTr 117
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
292 CCTCCATCCCAAGGAAGGGAGAGCGCTGTCCTCCAGCAGATTTAGCTG 341
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSerA 134
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
342 G..... 342
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
342 ..... 342
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
343 ..... 371
167 oMetAlaArgArg 171
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
372 CATAGCAAGACGC 384
seq_name: gb_ro:RATMBP
seq_documentation_block:
LOCUS      RATMBP      1464 bp      mRNA      ROD      27-APR-1993
DEFINITION rat myelin basic protein (mbp) gene mRNA.
ACCESSION  K00512
VERSION    K00512.1 GI:205320
KEYWORDS   rat (sprague dawley, newborn) cdna to brain mrna.
SOURCE     Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE  1 (bases 1 to 1464)
AUTHORS   Roach,A., Boylan,K.B., Horvath,S., Prusiner,S.B. and Hood,L.E.
TITLE     characterization of cloned cdna representing rat myelin basic
          protein: absence of expression in brain of shiverer mutant mice
          Cell 34, 799-806 (1983)
JOURNAL   MEDLINE 84026484
COMMENT   mbp's have been found in rats, small (m-r=14,000) and large
          (m-r=18,500). the sequence shown is for the small mbp, however the

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authors do not rule out one gene for both proteins.

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FEATURES             source
    Location/Qualifiers
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    /db_xref="taxon:10116"
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alignment_scores:
    Quality: 611.50      Length: 171
    Ratio: 4.777        Gaps: 3
Percent Similarity: 74.854 Percent Identity: 71.930

alignment_block:
US-09-218-277-12 x RATMBP ..
Align seg 1/1 to: RATMBP from: 1 to: 1464
1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
25 ATGGCATCACAGAGAGACCTCACAGCAGCGATCCAAGTACTTGGC 74
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
75 CACAGCAAGTACCATGAGCAGCATGCCGCGCATGCTTCTCCCAAGGCACA 124
|||||
34 rgAspThrGlyLeuLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
125 GAGACACGGGCATCTTGATCTCATCGCGCGCTCTTTAGCGGTGACAGG 174
|||||
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
|||||
175 GGTGCGCCCAAGCGGGCTCTGGCAGGAGCTACAC.....ACAAGAAC 218.
|||||
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
219 TACCCTACGGCTCCCTGCCCAAGAGTCGCAG...AGGACCCCAAGATG 265
|||||
84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
|||||
266 AAAACCCAGTAGTCCACTTCTTCAAGAACATGTGACACCTCGTACACC 315
|||||
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
|||||
316 CCTCATCTCCCAAGGAAGAGGAGAGGCGCTGCCCTCAGCAGATTAGCTG 365
|||||
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
|||||
366 G..... 366
|||||
134 sPtyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
|||||
366 ..... 366
|||||
151 LeuSerLysIlePheLysLeuGlyArgAspSerArgSerGlySerPr 167
|||||
367 .....GGAGGAAGAGACAGCGCGCTCTGGATCTCC 395
|||||
167 oMetAlaArgArg 171
|||||
396 CATAGCAAGACGC 408
|||||
seq_name: gb_ov:GMBP
seq_documentation_block:
LOCUS GMBP 2256 bp mRNA VRT 12-SEP-1993
DEFINITION Chicken mRNA for myelin basic protein.
ACCESSION X17103
VERSION X17103.1 GI:63594
KEYWORDS myelin basic protein.
SOURCE chicken.
ORGANISM Gallus gallus

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Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 2256)
Gundelfinger,E.D.
Direct Submission
Submitted (08-NOV-1989) Gundelfinger E. D., Universitaet Hamburg,
Universitaetskrankenhaus Eppendorf, Zentrum fuer Molekulare
Neurobiologie, Martinistrasse 52, 2000 Hamburg 20, FRG
2 (bases 1 to 2256)
Zopf,D., Sonntag,V., Betz,H. and Gundelfinger,E.D.
Developmental accumulation and heterogeneity of myelin basic
protein transcripts in the chick visual system
Glia 2 (4), 241-249 (1989)
MEDLINE 89358239
FEATURES             source
    Location/Qualifiers
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    /organism="Gallus gallus"
    /strain="white leghorn"
    /db_xref="taxon:9031"
    /dev_stage="day 1 post hatching"
    /tissue_type="brain optic lobe"
    /cell_type="oligodendrocytes"
    /clone_lib="lambda gt10"
    /clone="0219/10, 0219/2/3, 0219/2/2"
6. .530
    /note="myelin basic protein (AA 1-174)"
    /codon_start=1
    /protein_id="CAA34959.1"
    /db_xref="GI:63595"
    /db_xref="SWISS-PROT:P15720"
    /translation="MASKRSFRHSGKMASASTDTHARHSGPRHRSGLLDSLGREF
GGRHVPRRGFGRGDIHAARASHVSGIPQSRQHGRDDNPVHFKNIVSPRTPPMQ
AKGRGLSLTRFSGEGEHPGYSGKFEYEHKSAHKHKGSYHEGQGLSKIFKLGGSG
SRPGSRGSGSPVARR"
misc_feature 121
    /note="sequence polymorphism"
misc_feature 318..350
    /note="splice variant"
misc_feature 892..897
    /note="polyA signal"
misc_feature 912
    /note="processing variant"
misc_feature 1719
    /note="sequence polymorphism"
misc_feature 1812
    /note="sequence polymorphism"
misc_feature 2234..2239
    /note="polyA signal"
BASE COUNT      666 a   486 c   465 g   639 t
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alignment_scores:
    Quality: 603.50      Length: 178
    Ratio: 4.050        Gaps: 7
Percent Similarity: 83.708 Percent Identity: 69.101

alignment_block:
US-09-218-277-12 x GMBP ..
Align seg 1/1 to: GMBP from: 1 to: 2256
1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
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6 ATGGCTTCACAAAACGCTCCTTTCCGCGCAGGATCAAA...ATGCG 52
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
53 ATCGCAAGCACTACAGACCATGCTCGACATGA...TCTCCAAGGCACA 99
|||||
34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
100 GAGACTCGGGTCTACTTGACTCTCTGGCAGATCTTTGGAGGTGACAGA 149
|||||

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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
150 CACGTCCCGCGGGGGCTTTGGCAGGATATA...CAGCGAGCCAGGCG 196
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
67 rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGlnA 83
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
197 CAGCCATGTPAGGCTCCATCCCCCAGAGGTCCTCAGCATGCCCGCGCTGGTG 246
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
83 sPLuAsnProValValHisPhePheLysAsnIleValThrProArgThr 99
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
247 AGCACAACCCCTAGTCACCTCTTCAAGACATGTCCTCACCCGCTACT 296
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
100 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSe 116
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
297 CTTCTCCCAATCAAGCAAGGAGAGGACTGTCTCTCCACGATTTAG 346
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
116 rTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAla 133
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
347 CTGGGTGTGAAGGACACACAAAGCGGATACGGA...AGTGGAATTTCT 393
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
133 eAspTyrLysSerAlaHisLysGlyPheLysGlyVal.....AspAla 147
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
394 ATGAGCACAAATCTGCTCAAAAGGACACAAAGGATCTCTATCACGAGGCG 443
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
148 GlnGlyThrLeuSerLysLysPheLysLeuGlyGlyArg..... 160
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444 CAGGACACTCTTTCCAAATCTTTAACTGGGAGGCTGTGGCTCCCGGCC 493
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
161 .AspSerArgSerGlySerProMetAlaArgArg 171
   ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
494 TGGATCGCGGCTGTGGCTCACCAGTTCGAGAGGCG 527
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seq_name: gb_ro:RNO132896

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seq_documentation_block:
LOCUS      RNO132896      465 bp      mRNA      ROD      11-FEB-1999
DEFINITION Rattus norvegicus mRNA for myelin basic protein, 17 kDa isoform.
ACCESSION  AJ132896
VERSION    AJ132896.1  GI:4454312
KEYWORDS   isoform; mbp gene; myelin; myelin basic protein.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE  1 (bases 1 to 465)
AUTHORS   Lobell,A.M.
TITLE     Direct Submission
JOURNAL   Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
            Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
            SWEDEN
REFERENCE  2 (bases 1 to 465)
AUTHORS   Lobell,A.M. and Wigzell,H.
JOURNAL   Unpublished
FEATURES   Location/Qualifiers
            source          1..465
                        /organism="Rattus norvegicus"
                        /strain="Lewis rat"
                        /db_xref="taxon:10116"
            gene            1..465
                        /gene="mbp"
            CDS              1..465
                        /gene="mbp"
                        /note="17 kDa isoform"
                        /codon_start=1
                        /product="myelin basic protein"
                        /protein_id="CAA10805.1"
                        /db_xref="GI:4454313"
                        /translation="MASQKRPQRHSGSKYLATSTMDHARHGFLEPRHRTGILDSIGR
                        FFGDGRGAPKRGSKVPWLKQSRPLPSHARSFGLCKMYKDSHTRTHYGLSPQKQ
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BASE COUNT      117 a      153 c      120 g      75 t
ORIGIN

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    Ratio: 4.598        Gaps: 4
    Percent Similarity: 64.975      Percent Identity: 62.437

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US-09-218-277-12 x RNO132896
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Align seg 1/1 to: RNO132896 from: 1 to: 465

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1  ATGGGATCAGAGAGAGACCTCTCACGCGACACGGATCCAAGTACTTGGC 50
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
17  aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51  CACAGCAAGTACCATTGGACCATGCCCGCATGGCTTCCTCCCAAGGCACA 100
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
34  rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101  GAGACACGGGATCCTTGACTCCATCGGCGCTTCTTTAGCGGTGACAGG 150
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51  GlyAlaProLysArgGlySerGly..... 58
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151  GTTGGCCCCAAGCGGGGCTCTGGCAAGGTACCTGGCTAAAGCAGAGCGG 200
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
58  ..... 58

201  GAGCCCTCTGCTTCTCATGCCGAGCGGTCCTCCGCGGTGTGCCACATGT 250
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
59  ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251  ACAGGACTCACAC.....ACAAGACTAGCCACTACGGCTCCCTGCC 294
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
75  GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
295  CAGAAGTCCGACG...AGGACCCCAAGATGAAACCCAGTAGTCCACTTCT 341
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
91  eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
342  CAAGAACAATTGTGACACCTCTGACACCCCTCCATCCCAAGGAAGGGA 391
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
108  rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
392  GAGGCTGTCCCTCAGCAGATTTAGTGG..... 420
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
125  GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysGl 141
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420  ..... 420

141  yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
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421  .....G 421

158  lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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422  GAGGAAGAGACAGCGCGCTCTGGATCTCCCATAGCAAGACGC 462
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```

```
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
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301 CCCCGTCGCGAGGAAGGGAGAGGACTGCTCCCTGAGCAGATTAGCTG 350
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117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
|||||
351 GGGGCCCAAGCCAGACAGCAGGATTTGGCTACGGAGGCAGCGCTCG 400
|||||
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
|||||
401 ACTATAATCGCTCACAAGGATTCAGAGGAGTCGATGCCAGGGCAGC 450
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151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
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167 oMetaLysArg 171
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501 CATGGCTAGACGC 513

seq_name: N_Geneseq_36:T32561
seq_documentation_block:
ID T32561 standard; DNA; 516 BP.
AC T32561;
DT 07-NOV-1996 (first entry)
DE Human myelin basic protein (MBP) coding sequence.
KW Myelin basic protein; MBP; multiple sclerosis; MS; competition;
KW inhibition; major histocompatibility complex; MHC; thymocyte; T cell;
KW experimental allergic encephalomyelitis; EAE; analogue; treatment;
KW prevention; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 1..516
FT cds /tag= a
FT /product= Myelin basic protein.
PN W09616086-A1.
PD 30-MAY-1996.
PF 16-NOV-1995; U14403.
PR 18-NOV-1994; US-342408.
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
PI Conlon PJ, Gaur A, Ling N, Steinman L;
DR WPI; 96-268535/27.
DR P-PSDB; R99580.
PT Peptide analogues of human myelin basic protein - useful for
PT treatment of multiple sclerosis
PS Disclosure: Figure 1: 61pp; English.
CC Peptide analogues comprising at least seven amino acids from
CC residues 86-99 of human myelin basic protein (MBP), can be used to
CC treat multiple sclerosis by competing for the binding of native MBP
CC peptide to MHC and by not causing proliferation of an MBP reactive T-
CC cell line. The peptide analogues also inhibit the induction of
CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.
CC The peptide analogues have a reduced susceptibility to proteolysis
CC in vivo.
SQ Sequence 516 BP; 130 A; 153 C; 149 G; 84 T;

alignment_scores:
Quality: 922.00 Length: 171
Ratio: 5.392 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
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51 CACAGCAAGTACCATGGACCATGCCAGGATGGCTTCCTCCCAAGGCACA 100
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34 rGaspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
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101 GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTGGCGGTGACAGG 150
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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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151 GGTGCGCAAAAGCGGGCTCTGGCAAGGACTCACACCACCGCGCAAGAAC 200
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67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
201 TGTCTACTATGGCTCCCTGCCCAAGAGTCCACACGGCCGACCAAGATG 250
|||||
84 luAsnProValHisPhePheLysAsnIleValThrProArgThrPro 100
|||||
251 AAAACCCCGTAGTCCACTTCTCAAGAACATTTGTGACGCCCTCGACACCA 300
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101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
|||||
301 CCCCGTCGCGAGGAAGGGAGAGGACTGCTCCCTGAGCAGATTAGCTG 350
|||||
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
|||||
351 GGGGCCCAAGCCAGACAGCAGGATTTGGCTACGGAGGCAGCGCTCG 400
|||||
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
|||||
401 ACTATAATCGCTCACAAGGATTCAGAGGAGTCGATGCCAGGGCAGC 450
|||||
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
|||||
451 CTTTCCAAATTTTAAGCTGGGAGGAAGATAGTCGCTCTGGATCACC 500
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167 oMetaLysArg 171
|||||
501 CATGGCTAGACGC 513

seq_name: N_Geneseq_36:T41889
seq_documentation_block:
ID T41889 standard; cDNA to mRNA; 594 BP.
AC T41889;
DT 01-FEB-1997 (first entry)
DE Human myelin basic protein (foetal isoform) cDNA.
KW Myelin basic protein; MBP; MBP-X2Cys81; proteolipid protein;
KW PLP; multiple sclerosis; MBP; autoimmune disease; diagnosis; therapy;
KW T-lymphocyte; T-cell; anergy; apoptosis; ds.
OS Homo sapiens.
PN W09634622-A1.
PD 07-NOV-1996.
PF 22-APR-1996; U05611.
PR 02-MAY-1995; US-431648.
PR 02-MAY-1995; US-431644.
PR 07-JUN-1995; US-482114.
PA (ALEX-) ALEXION PHARM INC.
PA (USSR ) US DEPT HEALTH & HUMAN SERVICES.
PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
PI Nye SH, Peifrey CW, Squinto SP, Wilkins JA;
DR WPI; 96-505898/50.
DR P-PSDB; W00399.
PT New human myelin basic protein and proteolipid protein variant(s) -
PT used in the assessment, diagnosis and treatment of multiple
PT sclerosis
PS Claim 6; Page 79-80; 156pp; English.
CC A cDNA sequence (T41889) codes for the native human 21.5 kDa foetal
CC isoform (W00399) of myelin basic protein, MBP-X2Cys81/hum. This
CC isoform includes an exon 2-encoded region (X2) that may contain an
CC epitope involved in the pathogenesis of multiple sclerosis (MS); the
CC X2 region is not found in the MBP of healthy adults. The cDNA can be
CC obtd. by PCR amplification (see also T42785-90) and used to produce
CC recombinant MBP 21.5 in host, pref. bacterial, cells (see also
```

CC T41896-97). Recombinant MBP 21.5 polypeptides are useful in the
 CC clinical assessment, diagnosis and treatment of MS. 96 T;
 SQ Sequence 594 BP; 143 A; 184 C; 171 G; 96 T;

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 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:
 US-09-218-277-12 x T41889 ..

Align seg 1/1 to: T41889 from: 1 to: 594

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1 ATGGCGTCTCAGAGAGACCTCCAGAGGCACGGATCCAAAGTACCTGGC 50
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51 CACAGCAAGTACATGACCATGCCAGGATGCTTCTCCCAAGGCACA 100
|||||
34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
|||||
101 GAGACACGGGCATCTTGACTCATCGGGCGCTTCTTTGGCGGTGACAG 150
|||||
51 GlyAlaProLysArgGlySerGly..... 58
|||||
151 GGTGGCCCCAAGCGGGCTCTGGCAAGGTACCTGGCTAAAGCGGGCGG 200
58 ..... 58
201 GAGCCCTCTGCCCTCTCFATGCCCGCAGCCAGCGCTGGGCTGTGCAACATGT 250
|||||
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
251 ACAAGGACTCACACACCGCGCAGAGACTGCTCAGTATGGCTCCCTGGCC 300
|||||
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
|||||
301 CAGAAGTCACACGGCGCGGACCCCAAGATGAAACCCCGTAGTCCACTTCT 350
|||||
91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
|||||
351 CAAGAACAATTGTACGCCCTCGCACACACCCCGCTCGCAGGGAAAGGGA 400
|||||
108 rGglyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
|||||
401 GAGGACTGTCCCTGACACATTTAGTGGGGGCCCAAGGCCAGAGACCA 450
|||||
125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
|||||
451 GGATTGGCTACGAGGACGAGCGTCCGACTATAAATCGGCTCACAAGGG 500
|||||
141 yPheLysGlyValAspAlaGlnClyThrLeuSerLysIlePheLysLeuG 158
|||||
501 ATTCAAGGAGATGATGATGCCAGGGCAGCTTCCAAAATTTTCAAGCTGG 550
|||||
158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
|||||
551 GAGGAAGAGATAGTCTGCTCTGGATACCCATCCCATGCTAGACGC 591
|||||

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seq_name: N_Geneseq_36:T41896

seq_documentation_block:

ID T41896 standard; DNA; 612 BP.
 AC T41896;
 DT 01-FEB-1997 (first entry)
 DE Foetal myelin basic protein MBP+X2Cys81/bact. DNA.
 KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis; ds.

OS Synthetic.
 PN W09634622-A1.
 PD 07-NOV-1996. U05611.
 PF 22-APR-1996; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI; 96-505898/50.
 DR P-PSDB: W06107.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Disclosure; Page 81-82; 156pp; English.
 CC A DNA sequence (T41896) codes for the human 21.5 kDa foetal isoform
 CC (W06107) of myelin basic protein, MBP+X2Cys81/bact., and utilises
 CC bacterially-preferred codons in place of the native human codons
 CC (see also T41889). This increases prodn. of the MBP in E. coli by
 CC at least 50%. Recombinant MBP 21.5 polypeptides (see also W00399
 CC and W06108) are useful in the clinical assessment, diagnosis and
 CC treatment of MS.
 SQ Sequence 612 BP; 117 A; 215 C; 166 G; 114 T;

alignment_scores:

Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:

US-09-218-277-12 x T41896 ..

Align seg 1/1 to: T41896 from: 1 to: 612

```

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
1 ATGGCGTCTCAGAAACGTCGTCACGAGTCACGGCTCCAAATACCTGGC 50
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51 CACCGCAGCACCATGGACCATGCCGCTCATGGCTCTCTGGCGGTGACCG 100
|||||
34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
|||||
101 GTGACACGGGCATCTGGACTCCATCGCGCGCTTCTTCGGCGGTGACCG 150
|||||
51 GlyAlaProLysArgGlySerGly..... 58
|||||
151 GGTGGCGCCGAAACGTGGCTCTGGCAAGTGGCGTGAACACCGGGCGG 200
58 ..... 58
201 TAGCCCGCTGCCGTCTCATGCCCGTAGCCGCGCGGCTGTGCAACATGT 250
|||||
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
251 ACAAGACTCCCAACACCGCGCTCGTACCGGCACATATGGCTCCCTGGCG 300
|||||
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
|||||
301 CAGAAATCCACGGCGGTATCCAGGATGAAACCCCGGTGGTGGCTCTCT 350
|||||
91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
|||||
351 CAAAACATTTGTACCCCGCTACCCCGCGCGCTCTCAGGGCAAGGCC 400
|||||
108 rGglyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
|||||
401 GTGGCGCTGTCTGAGCCGCTTTCAGCTGGGGCGCGAAGGCCAGCGCTCG 450
|||||

```

125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 |||||
 451 GGCTTCGGTTACGGCGCGCTGCGTCCGACTATAAATCTGCTCACAAAGG 500
 |||||
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysLysIlePheLysLeuG 158
 |||||
 501 CTTCAAAAGCGTGGATGCCAGCGTACCTTGTCCAAAATTTTCAAACTGG 550
 |||||
 158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
 |||||
 551 GCGGCGGTGATACCGCTTCTGGCTCTCCGATGCTAGACGT 591
 |||||

seq_name: N_Geneseq_36:T41897

seq_documentation_block:
 ID T41897 standard; DNA; 612 BP.
 AC T41897;
 DT 01-FEB-1997 (first entry)
 DE Foetal myelin basic protein MBP-X2Ser81/bact.
 KW Myelin basic protein; MBP; MBP-X2Ser91; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis; ds.
 OS Synthetic.
 PN W0634622-Al.
 PD 07-NOV-1996.
 PF 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PR (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI: 96-505898/50.
 DR P-PSDB; W06108.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Disclosure: Page 82-83; 156pp; English.
 CC A DNA sequence (T41897) codes for the human 21.5 kDa foetal isoform
 CC (W06108) of myelin basic protein, MBP-X2Ser81/bact., and utilises
 CC codons that are preferentially used in highly-expressed bacterial
 CC genes and includes a sequence coding for an N-terminal hexa-
 CC histidine tag. This facilitates large-scale prodn. and purification
 CC of MBP 21.5 polypeptide in bacterial host cells. Recombinant MBP
 CC 21.5 polypeptides (see also W00399 and W06107) are useful in the
 CC clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 612 BP; 117 A; 215 C; 186 G; 114 T;

alignment_scores:
 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:

us-09-218-277-12 x T41897 ..

Align seg 1/1 to: T41897 from: 1 to: 612

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 |||||
 1 ATGCGGCTCAGAAACGCTCGCTCCAGCGTCACGGCTCCAAATACCTGGC 50
 |||||
 17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 |||||
 51 CACCGCCAGCAGCAGTACGACCATGCCCTCATGGCTTCTCGCGCGTCAAC 100
 |||||
 34 rGaspThrGlyIleLeuAspSerIleGlyArgPhePheGlyLysArg 50
 |||||
 101 GTGACACCGGCATCCTGGATCCATCGCGCGCTTCTTCGCGGTGACCGT 150
 |||||
 51 GlyAlaProLysArgGlySerGly..... 58
 |||||

151 GGTGCGCCGAAACGTGGCTCTGCAAAAGTGCCTGGCTGAAACCGGGCGG 200
 |||||
 58 58
 201 TAGCCCGCTGCCGCTCATGCGCGGTAGCCAGCGCGCTGTGCAACATGT 250
 |||||
 59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
 |||||
 251 ACAAGACATCCACACCGCGCTGTCGTCACCGCACATATGCTCCCTGCGG 300
 |||||
 75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
 |||||
 301 CAGAAATCCACGCGCGTACCAGGATGAAACCCCGTGGTGCACCTTCTT 350
 |||||
 91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
 |||||
 351 CAAAAACATGTGACCCCGCTACCCCGCGCGCTCTCAGGGCAAGGCC 400
 |||||
 108 rGlyLeuSerLeuSerArgPheSerTyrGlyAlaGluGlyGlnArgPro 124
 |||||
 401 GTGGCTGTCCCTGAGCCGTTTCAGCTGGGCGCGCAGGCGCGTCCG 450
 |||||
 125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 |||||
 451 GGCTTCGGTTACGGCGCGCTGCTCCGACTATAAATCTGCTCACAAAGG 500
 |||||
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysLysIlePheLysLeuG 158
 |||||
 501 CTTCAAAAGCGTGGATGCCAGCGTACCTTGTCCAAAATTTTCAAACTGG 550
 |||||
 158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
 |||||
 551 GCGGCGGTGATACCGCTTCTGGCTCTCCGATGCTAGACGT 591
 |||||

seq_name: N_Geneseq_36:T41893

seq_documentation_block:

ID T41893 standard; DNA; 1122 BP.

AC T41893;
 DT 01-FEB-1997 (first entry)
 DE MP4 chimera (MBP21.5-delta PLP4 fusion) DNA.
 KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;
 KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KW therapy; T-lymphocyte; T-cell; MP4 chimera; ds.
 OS Synthetic.
 PN W09634622-Al.
 PD 07-NOV-1996.
 PF 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PR (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI: 96-505898/50.
 DR P-PSDB; W06103.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 46; Page 110-112; 156pp; English.
 CC A DNA construct (T41893) codes for MP4 chimera (W06103), a fusion
 CC protein composed of human myelin basic protein (MBP) foetal isoform
 CC MBP21.5 (see also W00399) and delta PLP4 (W06101), a proteolipid
 CC protein (PLP) mutein that lacks all 4 hydrophobic domains of
 CC native human PLP (W06106) but includes PLP epitopes associated with
 CC multiple sclerosis (MS). It was constructed from DNA sequences
 CC encoding MBP21.5 (T41889) and delta PLP4 (T41891). The gene fusion
 CC in vector pMT22b was used to express MP4 in E. coli W3110 (DE3).
 CC PLP polypeptides (see also W00400, W06101-02 and W06104-05) can be
 CC used in the clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 1122 BP; 241 A; 354 C; 296 G; 231 T;

PF 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Mattis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI; 96-505898/50.
 DR P-PSDB; W06102.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 45; Page 108-110; 156pp; English.
 CC A DNA construct (T41892) codes for MP3 chimera (W06102), a fusion
 CC protein composed of human myelin basic protein (MBP) foetal isoform
 CC MBP21.5 (see also W00399) and delta PLP3 (W00400), a proteolipid
 CC protein (PLP) mutein that lacks hydrophobic domains 1, 3 and 4 of
 CC native human PLP (W06106) but includes PLP epitopes associated with
 CC multiple sclerosis (MS). It was constructed from DNA sequences
 CC encoding MBP21.5 (T41889) and delta PLP3 (T41890). The gene fusion
 CC in vector pET22b was used to express MP3 in E. coli W3110 (DE3).
 CC PLP polypeptides (see also W00400, W06101 and W06103-05) can be
 CC used in the clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 1155 BP; 239 A; 363 C; 306 G; 247 T;

alignment_scores:

Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:

US-09-218-277-12 x T41892 ..

Align seg 1/1 to: T41892 from: 1 to: 1155

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 |||||
 1 ATGCGCTCTCAGAAACGTCCGTCCTCCAGCGTCACGGCTCCAAATACCTGGC 50
 17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 |||||
 51 CACCGCCAGCACCACATGGACCATGCCCTCATGGCTTCTCGCCGCTCACC 100
 34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
 |||||
 101 GTGACACCGGCATCCTGGACTCCATCGCGCGCTTCTTCGGCGGTGACCGT 150
 51 GlyAlaProLysArgGlySerGly..... 58
 |||||
 151 GGTGCGCCGAAACGTGGCTCTGGCAAAAGTGCCTGGTGAACCGGGCCG 200
 58 58
 201 TAGCCCGCTGCCGTCTCATGCCCTAGCCAGCCGGGCTGTGCAACATGT 250
 59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
 |||||
 251 ACAAGACTCCACACCCCGGCTGTACCGGCGACTATGGCTCCCTGCCG 300
 75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
 |||||
 301 CAGAAATCCACACCGCGCTACCCAGGATGAAACCCGGTGGTGCACCTTCT 350
 91 eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGlyA 108
 |||||
 351 CAAAACATTTGTGACCCCGCGTACCCCGCGCGCTCTCAGGCGCAAGGCC 400
 108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
 |||||
 401 GTGCCCTGTCCCTGAGCGGTTTTCAGCTGGGGCCCGGAGGCCAGCGTCCG 450

alignment_scores:
 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:

US-09-218-277-12 x T41893 ..

Align seg 1/1 to: T41893 from: 1 to: 1122

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 |||||
 1 ATGCGCTCTCAGAAACGTCCGTCCTCCAGCGTCACGGCTCCAAATACCTGGC 50
 17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 |||||
 51 CACCGCCAGCACCACATGGACCATGCCCTCATGGCTTCTCGCCGCTCACC 100
 34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
 |||||
 101 GTGACACCGGCATCCTGGACTCCATCGCGCGCTTCTTCGGCGGTGACCGT 150
 51 GlyAlaProLysArgGlySerGly..... 58
 |||||
 151 GGTGCGCCGAAACGTGGCTCTGGCAAAAGTGCCTGGTGAACCGGGCCG 200
 58 58
 201 TAGCCCGCTGCCGTCTCATGCCCTAGCCAGCCGGGCTGTGCAACATGT 250
 59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
 |||||
 251 ACAAGACTCCACACCCCGGCTGTACCGGCGACTATGGCTCCCTGCCG 300
 75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
 |||||
 301 CAGAAATCCACACCGCGTACCCAGATGAAACCCGGTGGTGCACCTTCT 350
 91 eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGlyA 108
 |||||
 351 CAAAACATTTGTGACCCCGCGTACCCCGCGCGCTCTCAGGCGCAAGGCC 400
 108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
 |||||
 401 GTGCCCTGTCCCTGAGCGGTTTTCAGCTGGGGCCCGGAGGCCAGCGTCCG 450
 125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 |||||
 451 GCCTTCGGTTACGGCGCGGTGCGTCCGACATATAATCTGCTCACAAGG 500
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
 |||||
 501 CTTCAAAGCGGTGGATGCCAGGTACCTTGTCCAAATTTTCAAACCTGG 550
 158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
 |||||
 551 CGGCGCGTGATAGCGGTTCTGGCTCTCGATGGGTAGACGT 591

seq_name: N_Geneseq_36:T41892

seq_documentation_block:

ID T41892 standard; DNA; 1155 BP.
 AC T41892;
 DT 01-FEB-1997 (first entry)
 DE MP3 chimera (MBP21.5-delta PLP3 fusion) DNA.
 KW Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
 KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KW therapy; T-lymphocyte; T-cell; MP3 chimera; ds.
 OS Synthetic.
 PN WO9634622-A1.
 PD 07-NOV-1996.

125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 |||||
 451 GGCTTCGGTTACGGCGCGCTGCGTCCGACTATAAATCTGCTCACAAAG 500
 |||||
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
 |||||
 501 CTTCAAGGCGTGATGCCAGGCTACCTGTGCCAAATTTTCAAACTGG 550
 |||||

seq_name: N_Geneseq_36:T41895

seq_documentation_block:

ID T41895 standard; DNA: 1476 BP.

AC T41895;

DT 01-FEB-1997 (first entry)

DE MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion) DNA.

KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

KW therapy; T-lymphocyte; T-cell; MMOGP4 chimera;

KW myelin oligodendrocyte glycoprotein; MOG; ds.

OS Synthetic.

PN WO9634622-A1.

PD 07-NOV-1996.

PF 22-APR-1996; U05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

DR WPI; 96-505898/50.

DR P-PSDB; W06105.

PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis

PS Claim 48; Page 115-117; 156pp; English.

CC A DNA construct (T41895) codes for MMOGP4 chimera (W06105), a fusion
 CC protein composed of human myelin basic protein (MBP) foetal isoform
 CC MBP21.5 (see also W00399), the extracellular domain of human myelin
 CC oligodendrocyte glycoprotein (MOG) and delta PLP4 (W06101), a
 CC proteolipid protein (PLP) mutant that lacks all 4 hydrophobic
 CC domains of native human PLP (W06106) but includes PLP epitopes
 CC associated with multiple sclerosis (MS). It was constructed by
 CC inserting a sequence encoding the MOG moiety into MP4 chimera DNA
 CC (see also T41893) between the MBP and PLP derived sequences. The
 CC recombinant MMOGP4 chimera can be expressed in bacterial cell hosts.
 CC PLP polypeptides (see also W00400, W06101-03 and W06105) are useful
 CC in the clinical assessment, diagnosis and treatment of MS.

SQ Sequence 1476 BP; 332 A; 434 C; 403 G; 307 T;

alignment_scores:

Quality: 899.00 Length: 197

Ratio: 5.257 Gaps: 1

Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:

US-09-218-277-12 x T41895 ..

Align seg 1/1 to: T41895 from: 1 to: 1476

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 |||||
 1 ATGGCGTCTCAGAAAGCTCGTCCCGACGCTCAGGCTCCAAATACCTGGC 50
 |||||
 17 tThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 |||||
 51 CACCGCCAGACCATGACCATGCCCGCTCATGGCTTCTCCGCGCGTACC 100
 |||||

34 rGAspThrGlyIleLeuaspSerIleGlyArgPhePheGlyClyAspArg 50
 |||||
 101 GTGACACCGCATCTCGACTCCATCGCGCGCTTCTTCGGCGGTGACCGT 150
 |||||
 51 GlyAlaProLysArgLysSerGly..... 58
 |||||
 151 GTGCGCGCAACAGTGGCTCTGGCAAGTGGCGTGAACACGGCGCG 200
 |||||
 58 58
 201 TAGCCCGCTGCGCTCTCATGCCGTAGCCAGCGGCGCTGTGCAACATGT 250
 |||||
 59 ...LysAspSerHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
 |||||
 251 ACAAGACTCCCAACCGCGCTCGTACCGCGCACTATGGCTCCCTGCGC 300
 |||||
 75 GlnLysSerHisGlyArgThrGlnAspGluenProValValHisPhePh 91
 |||||
 301 CAGAATCCACGCGCGTACCCAGGATGAAACCCGCGGTGCACTTCTT 350
 |||||
 91 elysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
 |||||
 351 CAAAACATGTGACCGCGTACCCCGCGCTCTCAGGCGCAAGGCC 400
 |||||
 108 rGlyLysSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
 |||||
 401 GTGGCTGTCCCTGAGCGGTTTCAGTGGCGCGCAAGCGCGCGTCCG 450
 |||||
 125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 |||||
 451 GGCTTCGGTTACGGCGCGCTGCGTCCGACTATAAATCTGCTCAAAAGG 500
 |||||
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysLysIlePheLysLeuG 158
 |||||
 501 CTTCAAGGCGTGATGCCCGCGGTACCTGTGCCAAATTTTCAAACTGG 550
 |||||

seq_name: N_Geneseq_36:T41894

seq_documentation_block:

ID T41894 standard; DNA: 1125 BP.

AC T41894;

DT 01-FEB-1997 (first entry)

DE PM4 chimera (delta PLP4-MBP21.5 fusion) DNA.

KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

KW therapy; T-lymphocyte; T-cell; PM4 chimera; ds.

OS Synthetic.

PN WO9634622-A1.

PD 07-NOV-1996.

PF 22-APR-1996; U05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

DR WPI; 96-505898/50.

DR P-PSDB; W06104.

PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis

PS Claim 47; Page 113-114; 156pp; English.

CC A DNA construct (T41894) codes for PM4 chimera (W06104), a fusion

CC protein composed of delta PLP4 (W06101) and MBP21.5 (W00399).

CC Delta PLP4 is a proteolipid protein (PLP) mutant that lacks all 4

CC hydrophobic domains of native human PLP (W06106) but includes PLP

CC epitopes associated with multiple sclerosis (MS). MBP21.5 is a

CC foetal isoform of human myelin basic protein (MBP) associated with

CC MS. The DNA was constructed from sequences encoding delta PLP4
CC (T41891) and MBP21-5 (T41899). The gene fusion can be used to
CC express PM4 in bacterial hosts. PLP polypeptides (see also W00400,
CC W06101-03 and W06105) can be used in the clinical assessment,
CC diagnosis and treatment of MS.
SQ Sequence 1125 BP; 239 A; 359 C; 299 G; 228 T;

alignment_scores:
Quality: 894.00 Length: 196
Ratio: 5.259 Gaps: 1
Percent Similarity: 86.735 Percent Identity: 86.735

alignment_block:
US-09-218-277-12 x T41894 ..

Align seg 1/1 to: T41894 from: 1 to: 1125

2 AlaserGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAla18
|||||
520 GCGTCACAAACGTCGCGCCAGCTCAGCGCTCCAAATACCTGGCCAC 569
18 rAlaserThrMetAspHisAlaArgHisGlyPheLeuProArgHisArgA 35
|||||
570 CGCAGCACCATGACCATGCCGCTCATGCTTCCTGCGCGTCACCGTG 619
35 sPThrGlyLeuLeuAspSerIleGlyArgPheGlyGlyAspArgGly 51
|||||
620 ACACCGGCATCCTGGACTCCATCGCGCGCTTCTTCGCGGTGACCGTGT 669
52 AlaProLysArgGlySerGly..... 58
|||||
670 GCGCCGAAGCTGGCTCTGCAAGTGCCTGCTGCAACCGGGCGGTAG 719
59L 59
720 CCGCTGCCGTCTCATGCCGTAGCCAGCGCGGCTGTGCAACATGTACA 769
59 ysAspSerHisProAlaArgThrAlaHisTyrGlySerLeuProGln 75
|||||
770 AAGACTCCACACCGCGGTCTGACCGGCACCTATGCTCCCTGCGCGAG 819
76 LysSerHisGlyArgThrGlnAspGluAspProValValHisPhePhe 92
|||||
820 AATCCACCGCGGTACCCAGGATGAACCCGGTGTGCTCTCTCAA 869.
92 sAsnIleValThrProArgThrProProSerGlnGlyLysGlyArg 109
|||||
870 AATCATGTGACCCGCGGTACCCGCGCGCTCTCAGGGCAAGGCGGTG 919
109 lyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlnArgProGly 125
|||||
920 GCCTGCTCCTGAGCGGTTTCAGCTGGGCGCCGAGGCCAGCGTCCGGG 969
126 PheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGly 142
970 TTCGGTACCGCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1019
142 eLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuGly 159
|||||
1020 CAAAGCGGTGATGCCAGGCGACCTGTCCAAATTTTCAACTGGCGG 1069
159 lyArgAspSerArgSerGlySerProMetAlaArgArg 171
|||||
1070 GCGGTGATAGCGTTCGTGCTCTCCGATGCTAGACGT 1107

seq_name: N_Geneseq_36:Q48976

seq_documentation_block:

ID Q48976 standard; cDNA to mRNA; 1164 BP.
AC Q48976;
DT 18-APR-1994 (first entry)
DE Nucleotides 301-1464 of rat myelin gene.

KW RB35 antigen; Immunogen; myelin; rat; brain; antibody; IgG1; ds.
OS Rattus norvegicus.
PN J05219982-A.
PD 31-AUG-1993.
PF 07-FEB-1992; 055983.
PR 07-FEB-1992; JP-055983.
PA (TOKE) TOSHIBA KK.
DR WPI; 93-308342/39.
PT Monoclonal antibody against the proteins distributed in the brain
PT - is prepd. by using rat brain extract as immunogen belonging to
PT IgG1 class which combines to rat brain extract antigen
PS Claim 2; Page 2-3; 16pp; Japanese.
CC The rat myelin sequence hybridises to the closely similar
CC sequence coding for RB35 (Q48975). The RB35 sequence was isolated
CC from a cDNA library prepared from total adult female Sprague-Dawley
CC rat brain mRNA. RB35 protein is used as an immunogen to generate
CC monoclonal antibodies of the IgG1 subtype which specifically bind
CC to a protein in rat brain extract of mol.wt. ca. 30 kD.
SQ Sequence 1164 BP; 236 A; 335 C; 327 G; 266 T;

alignment_scores:
Quality: 160.00 Length: 76
Ratio: 4.444 Gaps: 1
Percent Similarity: 47.368 Percent Identity: 46.053

alignment_block:
US-09-218-277-12 x Q48976 ..

Align seg 1/1 to: Q48976 from: 1 to: 1164

96 ThrProArgThrProProSerGlnGlyLysGlyArgGlyLeuSerLe 112
|||||
1 ACACCTCGTACACCCCTCCATCCCAAGGAGGAGGCGCTGTCCCT 50
112 uSerArgPheSerTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrG 129
|||||
51 CAGCAGATTTAGCTGG..... 66
129 lyGlyArgAlaSerAspTyrLysSerAlaHisLysGlyPheLysGlyVal 145
66 66
146 AspAlaGlnGlyThrLeuSerLysIlePheLysLeuGlyGlyArgAspSe 162
|||||
67GGAGGAAGACACAG 80
162 rArgSerGlySerProMetAlaArgArg 171
|||||
81 CCGCTCTGGATCTCCATAGCAAGACGC 108

seq_name: N_Geneseq_36:Q48975

seq_documentation_block:

ID Q48975 standard; cDNA to mRNA; 1147 BP.
AC Q48975;
DT 18-APR-1994 (first entry)
DE Encodes RB35 protein from rat brain.
KW RB35 antigen; immunogen; myelin; Sprague-Dawley; rat; brain;
KW antibody; IgG1; ds.
OS Rattus norvegicus (Sprague-Dawley).
PN J05219982-A.
PD 31-AUG-1993.
PF 07-FEB-1992; 055983.
PR 07-FEB-1992; JP-055983.
PA (TOKE) TOSHIBA KK.
DR WPI; 93-308342/39.
PT Monoclonal antibody against the proteins distributed in the brain
PT - is prepd. by using rat brain extract as immunogen belonging to
PT IgG1 class which combines to rat brain extract antigen
PS Claim 2; Page 2-3; 16pp; Japanese.
CC The sequence coding for RB35 was isolated from a cDNA library
CC prepared from total adult female Sprague-Dawley rat brain mRNA.

CC RB35 is used as an immunogen to generate monoclonal antibodies
 CC of the IgG1 subtype which specifically bind to a protein in rat
 CC brain extract of mol.wt. ca. 30 kD.
 SQ Sequence 1147 BP; 261 A; 331 C; 329 G; 226 T;

alignment_scores:
 Quality: 135.00 Length: 71
 Ratio: 4.355 Gaps: 1
 Percent Similarity: 43.662 Percent Identity: 43.662

alignment_block:
 US-09-218-277-12 x Q48975/rev ..

Align seg 1/1 to reverse of: Q48975 from: 1 to: 1147

101 ProProSerGlnGlyLysGlyValArgGlyLeuSerArgPheSerTrp 117
 1143 CTCCATCCAGGAAAGGGAGGCGCTGCTCCATCAGCATTTAGCTG 1094
 117 polyAlaGluGlyGlnArgProGlyPheGlyTyrglyArgAlaSerA 134
 1093 G..... 1093
 134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
 1093 1093
 151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
 1092GGAGGAAGAGACACCCGCTCTGGATCTCC 1064
 167 oMetalaArgArg 171
 1063 CATGGCAAGAGCG 1051

seq_name: N_Geneseq_36:T47123

seq_documentation_block:

ID T47123 standard; cDNA; 621 BP.
 AC T47123;
 DT 11-SEP-1997 (first entry)
 DE cDNA encoding soluble fused MHC heterodimer:peptide complex pLJ13.
 KW Soluble; fusion; major histocompatibility complex; MHC;
 KW heterodimer; complex; antigen; binding groove; tolerance;
 KW autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
 KW antagonist; T cell; anergy; presenting cell; ds.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT mat_peptide 1..621 /*tag= a
 FT WO9640944-A2.
 PN 19-DEC-1996.
 PD 19-DEC-1996.
 PE 07-JUN-1996; U10102.
 PR 07-JUN-1995; US-482133.
 PR 07-JUN-1995; US-480002.
 PR 07-JUN-1995; US-483241.
 PR 27-OCT-1995; US-005964.
 PA (ANER-) ANERGEN INC.
 PA (ZYMO-) ZYMOGENETICS INC.
 PI Dashpande S, Gross JA, Kindsvogel W, Reich EP, Sheppard PO;
 DR WPI; 97-052337/05.
 DR P-PSDB; W10493.
 DR Novel fused major histocompatibility complex:antigenic peptide
 PT complex - useful to induce tolerance to an autoantigen-related
 PT disease e.g. insulin-dependent diabetes mellitus
 PS Example 1; Pages 118-119; 142pp; English.
 CC The present sequence encodes a novel soluble fused major
 CC histocompatibility complex (MHC) heterodimer:peptide complex,
 CC comprising 1st and 2nd MHC domains, linked by a 5-25 residue
 CC linker, and an antigenic peptide able to associate with a peptide
 CC binding groove of the MHC molecule, linked in frame to the 2nd

CC domain by a 5-25 residue linker. The complex can be used to induce
 CC immunological tolerance in adults susceptible to, or suffering from
 CC an autoantigen related disease, e.g. insulin dependent diabetes
 CC mellitus (IDDM), by antagonising the binding of particular T cells
 CC and antigen presenting cells, to induce anergy (immunological
 CC non-responsiveness) in the targeted T cell. As the heterodimers and
 CC corresponding antigen are permanently linked into a single chain,
 CC obviating the requirement for complex heterodimer truncation or
 CC formation, the complex eliminates inefficient and non-specific
 CC peptide loading.
 SQ Sequence 621 BP; 153 A; 148 C; 194 G; 126 T;

alignment_scores:

Quality: 134.00 Length: 37
 Ratio: 4.786 Gaps: 1
 Percent Similarity: 75.676 Percent Identity: 72.973

alignment_block:

US-09-218-277-12 x T47123 ..

Align seg 1/1 to: T47123 from: 1 to: 621

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99
 1 GACGAACCCAGCAGTAGTCACATCTTTAAACACATCGTACCGCGGTAC 50
 99 rProProSerGlnGly.....LysGlyArgGlyLeuSerLeuSerA 114
 51 ACCCCGCCATCGGAGCGGGTCAGTGATCGGGGACACCGGACCAC 100
 114 rgPheSerTrp 117
 101 GTTCTCTGTGG 111

seq_name: N_Geneseq_36:T67170

seq_documentation_block:

ID T67170 standard; DNA; 63 BP.
 AC T67170;
 DT 19-FEB-1998 (first entry)
 DE Human BPP-PE chimeric protein construction oligonucleotide Oligo 3.
 KW Pseudomonas exotoxin; myelin basic protein; chimeric protein;
 KW autoimmune disease; multiple sclerosis; human; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9719179-A1.
 PD 29-MAY-1997.
 PF 17-NOV-1996; IL0151.
 PR 26-DEC-1995; IL-116559.
 PR 17-NOV-1995; IL-116044.
 PA (YISS) YISSUM RES & DEV CO.
 PI Beraud E, Lorberboun-Galski H, Marianovsky I, Steinberger I;
 PI Yarkoni S;
 DR WPI; 97-298116/27.
 PT New Pseudomonas exotoxin-myeelin basic protein chimeric proteins -
 PT used for the treatment of autoimmune diseases, particularly
 PT multiple sclerosis
 PS Claim 7; Page 22; 54pp; English.
 CC New chimeric proteins have been developed comprising a Pseudomonas
 CC aeruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)
 CC moiety selected from: (a) MBP; (b) amino acids 69-88 of guinea-pig MBP
 CC or an antigenic portion; (c) amino acids 84-102 of human MBP or an
 CC antigenic portion; (d) amino acids 143-168 of human MBP or an antigenic
 CC portion; and (e) an amino acid sequence in which one or more amino acids
 CC have been deleted, added, substituted or mutated in the amino acid
 CC sequences of (a), (b), (c), or (d), the modified sequences retaining at
 CC least 75% homology with the amino acid sequences. The present sequence
 CC represents an oligonucleotide used for constructing human BPP-PE
 CC chimeric proteins. The chimeric proteins can be used for the treatment
 CC of autoimmune diseases such as multiple sclerosis. The chimeric proteins
 CC can specifically target and kill MBP specific T cells while having no
 CC effect on non-target cells.

SQ Sequence 63 BP; 21 A; 16 C; 7 G; 19 T;

alignment_scores:
Quality: 107.00 Length: 19
Ratio: 5.632 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x T67170 ..

Align seg 1/1 to: T67170 from: 1 to: 63

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99
|||||
5 GATGAATTCAGTAGTCATTTTAAATAATATTGTAACCCACGTAC 54

99 rProPro 101
|||||
55 CCCACCC 61

seq_name: N_Geneseq_36:T67171

seq_documentation_block:
ID T67171 standard; DNA; 63 BP.

AC T67171;
DT 19-FEB-1998 (first entry)
DE Human BPP-PE chimeric protein construction oligonucleotide Oligo 5.
KW Pseudomonas exotoxin; myelin basic protein; chimeric protein;
OS autoimmune disease; multiple sclerosis; human; ss.

OS Synthetic.
PN WO9719179-A1.
PD 29-MAY-1997.

PF 17-NOV-1996; IL0151.

PR 26-DEC-1995; IL-116559.

PR 17-NOV-1995; IL-116044.

PA (YISS) YISSUM RES & DEV CO.

PI Beraud E, Lorberboun-Galski H, Marianovsky I, Steinberger I;
PI Yarkoni S;

DR WPI; 97-298116/27.

PT New Pseudomonas exotoxin-myein basic protein chimeric proteins -
PT used for the treatment of auto-immune diseases, particularly

PT multiple sclerosis

PS Claim 7; Page 22; 54pp; English.

CC New chimeric proteins have been developed comprising a Pseudomonas
CC aeruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)
CC moiety selected from: (a) MBP; (b) amino acids 69-88 of guinea-pig MBP
CC or an antigenic portion; (c) amino acids 84-102 of human MBP or an
CC antigenic portion; (d) amino acids 143-168 of human MBP or an antigenic
CC portion; and (e) an amino acid sequence in which one or more amino acids
CC have been deleted, added, substituted or mutated in the amino acid
CC sequences of (a), (b), (c), or (d), the modified sequences retaining at
CC least 75% homology with the amino acid sequences. The present sequence
CC represents an oligonucleotide used for constructing human BPP-PE
CC chimeric proteins. The chimeric proteins can be used for the treatment
CC of autoimmune diseases such as multiple sclerosis. The chimeric proteins
CC can specifically target and kill MBP specific T cells while having no
CC effect on non-target cells.

SQ Sequence 63 BP; 21 A; 15 C; 8 G; 19 T;

alignment_scores:
Quality: 107.00 Length: 19
Ratio: 5.632 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x T67171 ..

Align seg 1/1 to: T67171 from: 1 to: 63

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99

|||||
5 GATGAATTCAGTAGTCATTTTAAATAATATTGTAACCCACGTAC 54

99 rProPro 101
|||||
55 CCCACCC 61

seq_name: N_Geneseq_36:T67168

seq_documentation_block:
ID T67168 standard; DNA; 63 BP.

AC T67168;

DT 19-FEB-1998 (first entry)

DE BPP-PE chimeric protein synthesis oligonucleotide Oligo 3.

KW Pseudomonas exotoxin; myelin basic protein; chimeric protein;

KW autoimmune disease; multiple sclerosis; human; ss.

OS Synthetic.

PN WO9719179-A1.

PD 29-MAY-1997.

PF 17-NOV-1996; IL0151.

PR 26-DEC-1995; IL-116559.

PR 17-NOV-1995; IL-116044.

PA (YISS) YISSUM RES & DEV CO.

PI Beraud E, Lorberboun-Galski H, Marianovsky I, Steinberger I;
PI Yarkoni S;

DR WPI; 97-298116/27.

PT New Pseudomonas exotoxin-myein basic protein chimeric proteins -
PT used for the treatment of auto-immune diseases, particularly

PT multiple sclerosis

PS Claim 7; Page 9; 54pp; English.

CC New chimeric proteins have been developed comprising a Pseudomonas
CC aeruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)
CC moiety selected from: (a) MBP; (b) amino acids 69-88 of guinea-pig MBP
CC or an antigenic portion; (c) amino acids 84-102 of human MBP or an
CC antigenic portion; (d) amino acids 143-168 of human MBP or an antigenic
CC portion; and (e) an amino acid sequence in which one or more amino acids
CC have been deleted, added, substituted or mutated in the amino acid
CC sequences of (a), (b), (c), or (d), the modified sequences retaining at
CC least 75% homology with the amino acid sequences. The present sequence
CC represents an oligonucleotide used in the synthesis of BPP-PE chimeric
CC proteins. The chimeric proteins can be used for the treatment of
CC autoimmune diseases such as multiple sclerosis. The chimeric proteins
CC can specifically target and kill MBP specific T cells while having no
CC effect on non-target cells.

SQ Sequence 63 BP; 21 A; 15 C; 8 G; 19 T;

alignment_scores:
Quality: 107.00 Length: 19
Ratio: 5.632 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x T67168 ..

Align seg 1/1 to: T67168 from: 1 to: 63

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99

|||||
5 GATGAATTCAGTAGTCATTTTAAATAATATTGTAACCCACGTAC 54

99 rProPro 101
|||||
55 CCCACCC 61

OM of: US-09-218-277-12 to: Issued Patents_NA: * out_format : pfs

Date: Sep 26, 2000 8:02 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-B=Issued Patents_NA -QFMT=fastap -SUFFIX=rn1 -GAPOP=12.000  
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Search length: 68777915  
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Sequence 4, Application PC/TUS9605611A

GENERAL INFORMATION:

APPLICANT: Mueller, John P.

APPLICANT: Leonardo, Michael J.

APPLICANT: McFarland, Henry F.

APPLICANT: Mettis, Louis A.

APPLICANT: Mueller, Eileen Elliott

APPLICANT: Nye, Steven H.

APPLICANT: Pelfrey, Clara M.

APPLICANT: Squinto, Stephen P.

APPLICANT: Wilkins, James A.

TITLE OF INVENTION: Modified Myelin Protein Molecules

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maurice M. Klee

STREET: 1951 Burr Street

CITY: Fairfield

STATE: Connecticut

COUNTRY: USA

ZIP: 06430

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 0.8 Mb storage

COMPUTER: Macintosh Centris 610

OPERATING SYSTEM: System 7

SOFTWARE: Microsoft Word 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/05611A

FILING DATE: 02-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/431,644

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/431,648

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/482,114

FILING DATE: June 7, 1995

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ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Human 18.5 kDa form of MBP
HYPOTHETICAL: No
ANTI-SENSE: No
PCT-US96-05611A-4

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: GENERAL INFORMATION:
: APPLICANT: Mueller, John P.
: APPLICANT: Leonardo, Michael J.
: APPLICANT: McFarland, Henry F.
: APPLICANT: Matis, Louis A.
: APPLICANT: Mueller, Eileen Elliott
: APPLICANT: Nye, Steven H.
: APPLICANT: Peltrey, Clara M.
: APPLICANT: Squinto, Stephen P.
: APPLICANT: Wilkins, James A.
: TITLE OF INVENTION: Modified Myelin Protein Molecules
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESS: Maurice M. Klee
: STREET: 1951 Burr Street
: CITY: Fairfield
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06430
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
: COMPUTER: Macintosh Centris 610
: OPERATING SYSTEM: System 7
: SOFTWARE: Microsoft Word 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/05611A
: FILING DATE: 02-MAY-1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/431,644
: FILING DATE: May 2, 1995
: APPLICATION NUMBER: 08/431,648
: FILING DATE: May 2, 1995
: APPLICATION NUMBER: 08/482,114
: FILING DATE: June 7, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Klee, Maurice M.
: REGISTRATION NUMBER: 30,399
: REFERENCE/DOCKET NUMBER: ALX-129
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203) 254 1400
: TELEFAX: (203) 254 1101
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 594 base pairs
: TYPE: Nucleic acid
: STRANDEDNESS: Double
: TOPOLOGY: Linear
: MOLECULE TYPE: cDNA to mRNA
: DESCRIPTION: MBP-X2Cys81/num. (Human 21.5 kd form
: DESCRIPTION: of MBP)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: PUBLICATION INFORMATION:
: AUTHORS: Roth, H. J.
: AUTHORS: Kronquist, K. E.
: AUTHORS: Kerlero de Rosbo, N.
: AUTHORS: Grandall, B. F.
: AUTHORS: Campagnoni, A. T.
: TITLE: Evidence for the Expression of Four
: TITLE: Myelin Basic Protein Variants in the
: TITLE: Developing Human Spinal Cord Through
: TITLE: cDNA Cloning
: JOURNAL: Journal of Neuroscience Research
: VOLUME: 17
: PAGES: 312 - 328
: DATE: 1987
: PCT-US96-05611A-1

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seq_documentation_block:
: Sequence 2, Application PC/TUS9605611A
: GENERAL INFORMATION:
: APPLICANT: Mueller, John P.
: APPLICANT: Leonardo, Michael J.
: APPLICANT: McFarland, Henry F.
: APPLICANT: Matis, Louis A.
: APPLICANT: Mueller, Eileen Elliott
: APPLICANT: Nye, Steven H.
: APPLICANT: Peltrey, Clara M.
: APPLICANT: Squinto, Stephen P.

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APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 MB storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: MBP+X2Ys81/Dact.
HYPOTHEtical: NO
ANTI-SENSE: NO
PCT-US96-05611A-2

Alignment_scores:
Quality: 899.00 Length: 197
Ratio: 5.257 Gaps: 1
Percent Similarity: 86.802 Percent Identity: 86.802

Alignment_block:
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Align seg 1/1 to: PCT-US96-05611A-2 from: 1 to: 612

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seq_documentation_block:
Sequence 3: Application PC/TUS9605611A
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Leonardo, Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Mattis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 MB storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399


```

REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: MBP-X2Ser81/bact.
HYPOTHETICAL: No
ANTI-SENSE: No
PCT-US96-05611A-3

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alignment_scores:
Quality: 899.00      Length: 197
Ratio: 5.257        Gaps: 1
Percent Similarity: 86.802      Percent Identity: 86.802

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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-3 ..

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Align seg 1/1 to: PCT-US96-05611A-3 from: 1 to: 612

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1 ATGGCGTCTCAGAAAGCTCCGTCACGCGTCCAGGCTCCCAAAATCCTGGC 50
|||||
17 aThAlaSerThrMetAspHisAlaArgHISgLyPheLeuProArgHISa 34
|||||
51 CACCGCCACACCATGACCATGCCGCTGCTGCGCGCTGACCG 100
|||||
34 rGAspThrLylleLeuAspSerLleGlyArgPheGlyLysArgParg 50
|||||
101 GTGACACCGGCATCTGACCTCATGGCGCTTCTTCGGGTGACCG 150
|||||
51 GtAlAProLysArggLySerLy..... 58
|||||
151 GGTGCCCGCAAGCTGCTCTGGCAAGTGCCTGGCTGAACCGGGCGG 200
|||||
58 ..... 58
201 TAGCCCGCTGCGCTCATGCCCGTAGCCAGCGGGCCTGTGCAACATG 250
|||||
59 .. LysAspSerHISHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
251 ACAAAAGACTCCACACCGCGGCTCGTACCGCGCATATGCTCCCTGCCG 300
|||||
75 GlnLysSerHISgLyArgThrGlnAspGluAsnProValAlaHisPheP 91
|||||
301 CAGAAATCCACGCGCGCTACCCAGGATGAAGAACCCGCTGTCACATCTT 350
|||||
91 eLysAsnIleValThrProArgThrProProProSerGlnLysGlyAla 108
|||||
351 CAAAACATGTGACCCCGCGTACCCCGCGCGCTCTCAGGCGAAAGGCC 400
|||||
108 rGgLyLeuSerLeuSerArgPheSerTyrGlyAlaGluGlyGlnArgPro 124
|||||
401 GTGGCGTGTCCCTGAGCCGCTTTCAGCTGGGGCGCCGAAAGGCCGCTCC 450
|||||
125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisTysg 141
|||||
451 GGCTTGGGTACGGCGCGCGCTGGCTCGCATTAATCTGCTACAAAGG 500
|||||
141 yPheLysGlyValAlaSPalagInGlyThrLeuSerLysIlePheLysLeu 158
|||||
501 CTTCAAAGGGGTGATGCCAGGGGTACCTGTCCAAATTTTCAAACTGG 550
|||||
158 LysLysArgAspSerArgSerGlySerProMetAlaArgArg 171
|||||

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551 GCGGCCGTGATAGCCGCTCTGCGCTCCGATGCTAGACGT 591

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seq_name: /cgn1_7/ptodata/1/lna/PCTUS-COMB.seq:PCT-US96-05611A-26

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seq_documentation_block:

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Sequence 26, Application PC/TUS9605611A

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```

GENERAL INFORMATION:

```

```

APPLICANT: Mueller, John P.

```

```

APPLICANT: Leonardo, Michael J.

```

```

APPLICANT: McFarland, Henry F.

```

```

APPLICANT: Matis, Louis A.

```

```

APPLICANT: Mueller, Eileen Elliott

```

```

APPLICANT: Nye, Steven H.

```

```

APPLICANT: Pelfrey, Clara M.

```

```

APPLICANT: Squinto, Stephen P.

```

```

APPLICANT: Wilkins, James A.

```

```

TITLE OF INVENTION: Modified Myelin Protein Molecules

```

```

NUMBER OF SEQUENCES: 29

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Maurice M. Klee

```

```

STREET: 1951 Burr Street

```

```

CITY: Fairfield

```

```

STATE: Connecticut

```

```

COUNTRY: USA

```

```

ZIP: 06430

```

```

COMPUTER READABLE FORM:

```

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MEDIUM TYPE: 3.5 inch, 0.8 Mb storage

```

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COMPUTER: Macintosh Centris 610

```

```

OPERATING SYSTEM: System 7

```

```

SOFTWARE: Microsoft Word 6.0.1

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```

CURRENT APPLICATION DATA:

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```

APPLICATION NUMBER: PCT/US96/05611A

```

```

FILING DATE: 02-MAY-1995

```

```

CLASSIFICATION:

```

```

PRIORITY APPLICATION DATA:

```

```

APPLICATION NUMBER: 08/431,644

```

```

FILING DATE: May 2, 1995

```

```

APPLICATION NUMBER: 08/431,648

```

```

FILING DATE: May 2, 1995

```

```

APPLICATION NUMBER: 08/482,114

```

```

FILING DATE: June 7, 1995

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: Klee, Maurice M.

```

```

REGISTRATION NUMBER: 30,399

```

```

REFERENCE/DOCKET NUMBER: ALX-129

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: (203) 255 1400

```

```

TELEFAX: (203) 254 1101

```

```

INFORMATION FOR SEQ ID NO: 26:

```

```

SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 1122 base pairs

```

```

TYPE: Nucleic acid

```

```

STRANDEDNESS: Double

```

```

TOPOLOGY: Linear

```

```

MOLECULE TYPE: Other nucleic acid

```

```

DESCRIPTION: MP4 chimera

```

```

HYPOTHETICAL: No

```

```

ANTI-SENSE: No

```

```

PCT-US96-05611A-26

```

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alignment_scores:

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Quality: 899.00      Length: 197
Ratio: 5.257        Gaps: 1
Percent Similarity: 86.802      Percent Identity: 86.802

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alignment_block:

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US-09-218-277-12 x PCT-US96-05611A-26 ..

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Align seg 1/1 to: PCT-US96-05611A-26 from: 1 to: 1122

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1 MetAlaSerGlnLysArgProSerGlnArgHISgLySerLysTyrLeuAl 17
|||||

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1 ATGCGCTCTCGAAGACGTCCCTCCAGCGTACGGCTCCAAATACCTGGC 50
17 aThAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
51 CACGGCCAGCAGCATGGACATGCGCGCATGCTTCTCGCGGTACCC 100
34 rGaApThrGlyIleLeuAspSerIleGlyArgPhePheGlyAspArg 50
101 GTGACACCGGCGATCTGTGACTGCATCGCGCTTCTCGGGGTGACCGT 150
51 gLyAlaProLysArgGlySerGly..... 58
151 GGTGCGCGGAACGTGGCTCTGGCAAGTGGCGGTGCTGAAACCGGGCG 200
58 ..... 58
201 TAGCCCGCTGCGCTCTCATGCCGATGCCAGCCGGGCGCTGTGCAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGAGACTCCACACCGCGCTGTACCGCGCACTATGCTCCCTGCGC 300
75 gLnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
301 CAGAAATCCACGCGCGCTACCCAGATGAAACCGGGTGTGCACTTCTT 350
91 eLysAsnIleValThrProArgThrProProProSerGlnGlyAspArg 108
351 CAAAAACATTGTGACCCCGCGCTACCGCGCGCGCTCAGGGCAAGGCC 400
108 rGgLyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
401 GTGGCTGTCTCCCTAGCGCTTTCAGCTGGGGCGCGGAAGGCGACGCTCG 450
125 gLyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisTylsG 141
451 GCGTTCGGTTACGGCGCGCGCTGCTCCGACTATTAATGTGCTCACAAGG 500
141 yPheLysGlyValAlaSpAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
501 CTTCAAGGCGGTGATGCCCGAGGAGTACTTGTCCAAATTTTCAACGCG 550
158 lYgLyArgAspSerArgSerGlySerProMetAlaArg 171
551 GCGGCCGTGATAGCGCTTCTGCTCGATGCGTAGACGT 591
seq_name: /cgnl_7/prodata/1/lna/pctus_comb.seq:pct-US96-05611A-25
seq_documentation_block:
; Sequence 25, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 MB storage
; COMPUTER: Macintosh Centris 610
; OPERATING SYSTEM: System 7

```

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; SOFTWARE: Microsoft Word 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05611A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,644
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/431,648
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/482,114
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: MP3 chimera
; HYPOTHEICAL: No
; ANTI-SENSE: No
; PCT-US96-05611A-25

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alignment_scores:

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Quality: 899.00 Length: 197
Ratio: 5.257 Gaps: 1
Percent Similarity: 86.802 Percent Identity: 86.802

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alignment_block:

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US-09-218-277-12 x PCT-US96-05611A-25 ..

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Align seg 1/1 to: PCT-US96-05611A-25 from: 1 to: 1155

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1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
1 ATGCGCTCTCGAAGACGTCCCTCCAGCGTACGGCTCCAAATACCTGGC 50
17 aThAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51 CACGGCCAGCAGCATGGACATGCGCGCATGCTTCTCGCGGTACCC 100
34 rGaApThrGlyIleLeuAspSerIleGlyArgPhePheGlyAspArg 50
|||||
101 GTGACACCGGCGATCTGTGACTGCATCGCGCTTCTCGGGGTGACCGT 150
51 gLyAlaProLysArgGlySerGly..... 58
|||||
151 GGTGCGCGGAACGTGGCTCTGGCAAGTCCGCTGCTGAAACCGGGCG 200
58 ..... 58
201 TAGCCCGCTGCGCTCTCATGCCGATGCCAGCCGGGCGCTGTGCAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
251 ACAAGAGACTCCACACCGCGCTGTACCGCGCACTATGCTCCCTGCGC 300
75 gLnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
|||||
301 CAGAAATCCACGCGCGCTACCCAGATGAAACCGGGTGTGCACTTCTT 350
91 eLysAsnIleValThrProArgThrProProProSerGlnGlyAspArg 108
|||||
351 CAAAAACATTGTGACCCCGCGTACCGCGCGCTCAGGGCAAGGCC 400

```

```

108  rgglyleuSerleuSerArpPheSerTrpGlyAlaGluGlyAlaArgPro 124
      |||||||
401  GTGGGCTCTCCCTGAGCCGTTTCAGCTGGGGCGGAGGCCGCGTCCG 450
125  glyPheGlyTrpGlyAlaArgAlaSerAspTyrLysSerAlaHisLysG1 141
      |||||||
451  GGCTTCGGTTACGGCGCGGCGTCCGACTTAAATCTGCTCACAAGG 500
141  yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
      |||||||
501  CTTCAAGAGCGGTGATGCCAGGACTTGTCCAAATTTTCAACACGCG 550
158  lyGlyArgAspSerArgSerGlySerPrometAlaArg 171
      |||||||
551  GCGGCGGTGATAGCCGTTCTGCTCTCCGATGCGTAGACGT 591

seq_name: /cgnl_7/prodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-28

seq_documentation_block:
; Sequence 28, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Sculinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 mb storage
; COMPUTER: Macintosh Centris 610
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05611A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,644
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/431,648
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/482,114
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1476 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: MMOGP4 chimera
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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PCT-US96-05611A-28

alignment_scores:
      Quality: 899.00      Length: 197
      Ratio: 5.257
      Percent Similarity: 86.802      Percent Identity: 86.802

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-28 ..
Align seg 1/1 to: PCT-US96-05611A-28 from: 1 to: 1476

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
1 ATGGGGGTCTCAGAAACGTCCTCCACAGGTGACAGGCTCCAAATACCTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
51 CACGCGCACACATGACATGCCCGCTCATGGCTTCTGCGCGGTCCACC 100
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyLysArg 50
101 GTGACACCGCGCATCTGACTTCATCGGCCCTTCTTGGCGGTGACCGT 150
51 G1AlaProLysArgLysGly..... 58
151 GTGGGCGCGAAGCGGTCTGGCAAGTGCGCGGTGAAACCGGGCGG 200
58 ..... 58
201 TAGCCCGCTGCGTCTCATGCCGTAGCCAGCCGGCGCTGTCAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGAGCTCCACACCCCGGCTGTGACCGCACATAGGCTCCCTGGCG 300
75 GlnLysSerHisGlyArgThrGlnAspGlnAsnProValAlaHisPhePh 91
301 CAGAAATCCACAGGCGGTACCCAGATGAACCGGCGGTGACTTCTT 350
91 eLysAsnIleValHisProArgThrProProProSerGlnLysGlyA 108
351 CAAAACATTTGTGACCCCGCTACCCGCCCGCTCTCAGGCGCAAGGCC 400
108 rgglyleuSerleuSerArpPheSerTrpGlyAlaGluGlyAlaArgPro 124
401 GTGGCTCTCCCTGAGCCGTTTCAGCTGGGGCGGAGGCCGACCGTCCG 450
125 glyPheGlyTrpGlyAlaArgAlaSerAspTyrLysSerAlaHisLysG1 141
451 GGCTTCGGTTACGGCGCGGCGTCCGACTTAAATCTGCTCACAAGG 500
141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
501 CTTCAAGAGCGGTGATGCCAGGACTTGTCCAAATTTTCAACACGCG 550
158 lyGlyArgAspSerArgSerGlySerPrometAlaArg 171
551 GCGGCGGTGATAGCCGTTCTGCTCTCCGATGCGTAGACGT 591

seq_name: /cgnl_7/prodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-27

seq_documentation_block:
; Sequence 27, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.

```

APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PM4 chimera
HYPOTHEICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-27
alignment_scores:
Quality: 894.00 Length: 196
Ratio: 5.259 Gaps: 1
Percent Similarity: 86.735 Percent Identity: 86.735
alignment_block:
US-09-218-277-12 x PCT-US96-05611A-27 ..
Align seq 1/1 to: PCT-US96-05611A-27 from: 1 to: 1125
2 AIsSerGlnIysAlrGProSerGlnAlrGHisGlySerIysTyrLeuAlaTh 18
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520 GCGTCTCAGAAAGTCGCTCCAGCGCAGCGCTCCCAATATACCTGGCCAC 569
18 fAlaserThMetAspHisAlaArgHisGlyPheLeuProAlrGHisArg 35
|||||
570 CGCGACGACCATGACCATGCCGTCTATGGCTTCCTGCCGCGTCACCGTG 619
35 sPhrGlyIleLeuAspSerIleGlyArpPheGlyIysIAspArgGly 51
|||||
620 ACACCGGACATCTGGACTCCATGGCGCGCTTCTTCGCGGTGACCGTGT 669
52 AlAlProIysArgIysSerGly..... 58
670 GCCCGCAAGCGTGCTCTGCGCAAGTCCGTGGGTGAAACGGGCGGTAG 719

59L 59
720 CCCGTCGCGTCTCATGCCCCGAGCCAGCGGCGCTGTCCAACTGATACA 769
59 yAspSerHisHisProAlaArgThrAlaHisIleTyrGlySerLeuProGln 75
|||||
770 AGACTCCACACCCAGCGGCTGTGACCGGCACATATGCTCCCTGCCGCG 819
76 LysSerHisGlyArGThrGlnAspGluAsnProValAlaHisPhePhe 92
|||||
820 AAATCCACGCGCGGTACCCAGATGAAGAACCGGTGTGCTCACTTTCAA 869
92 sAsnIleValThrProArgThrProProProSerGlnGlyIysGlyArg 109
|||||
870 AAACATGTGACCCCGCGTACCCCGCGCGCTCTCAGGGCAAGGCGCGTG 919
109 lYLeuSerLeuSerArgPheSerTyrPglYAlaGluIysIAspArgProGly 125
|||||
920 GCGTGTCCCTGAGCCCTTTCAGCTGGGGCGCCGAAGGCCAGCGTCCGGCG 969
126 PheGlyTyrGlyGlyArGAlaSerAspTyrIysSerAlaHisIysGlyPh 142
|||||
970 TTCGGCTACGGCGCGCGCTGCGTCCGACTATAATCTGTACAAAGGCTT 1019
142 eIysGlyValAspAlaGlnGlyThrLeuSerIysIlePheIysLeuGly 159
|||||
1020 CAAAGCGGTGATGCCAGGCGCACCTGTCCAAATTTTCAAACTGGGCG 1069
159 lYArGAspSerArgSerGlySerProMetAlaArgArg 171
|||||
1070 GCCGTATAGCCGCTTGTGCTCTCCGATGCTAGACGT 1107
seq.name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq: PCT-US96-05611A-8
seq.documentation_block:
; Sequence 8, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
; COMPUTER: Macintosh Centris 610
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05611A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,644
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/431,648
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/482,114
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.

```

;
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 bases
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: PCR primer oligonucleotide 4
; HYPOTHEICAL: No
; ANTI-SENSE: Yes
; PCT-US96-05611A-8

alignment_scores:
      Quality: 236.00      Length: 43
      Ratio: 5.488      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-8/rev ..

Align seg 1/1 to reverse of: PCT-US96-05611A-8 from: 1 to: 131

77 SerHisGlyArgThrGlnAspGluAsnProValValHisPhePheLysAs 93
|||||
130 TCCAGGCGCCGATACCAAGATGAAGCCGCGTGTCTCTTCAAAAA 81

93 nileValThrProArgThrProProSerGlnGlyLysGlyArgGlyL 110
|||||
80 CATTGAGACCCCGCTACCCCGCGCTCTCAGGCCAAGCGCGTGGCC 31

110 euseSerArgPheSerTrpGlyAla 119
|||||
30 TGTCCCTGAGCCGTTTCAGCTGGGGCGCC 2

seq_name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-9

seq_documentation_block:
; Sequence 9, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
; COMPUTER: Macintosh Centris 610
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05611A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

```

;
; APPLICATION NUMBER: 08/431,644
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/431,648
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/482,114
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 bases
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: PCR primer oligonucleotide 5
; HYPOTHEICAL: No
; ANTI-SENSE: No
; PCT-US96-05611A-9

alignment_scores:
      Quality: 214.00      Length: 39
      Ratio: 5.487      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-9 ..

Align seg 1/1 to: PCT-US96-05611A-9 from: 1 to: 119

114 ArgPheSerTrpGlyAlaGluGlnArgProGlyPheGlyTyrglyc 130
|||||
3 CGTTTCAGCTGGGGCGCCGAGAGCCAGCGTCCGGCTTGGCTACGGCGG 52

130 yArgAlaSerAspTyrLysSerAlaHisLysGlyPheLysGlyValAsp 147
|||||
53 CCGTGGCTCCGACTATTAATCTGTCACAAAGGCTTCAAGCGGTGAG 102

147 lagInglyThrLysSer 152
|||||
103 CCCAGGCGACCTGTCC 119

seq_name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-5

seq_documentation_block:
; Sequence 5, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 Mb storage

```

```
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-5
```

```
alignment_scores:
Quality: 188.00      Length: 35
Ratio: 5.371         Gaps: 0
Percent Similarity: 100.000    Percent Identity: 100.000
```

```
alignment_block:
US-09-218-277-12 x PCT-US96-05611A-5 ..
```

```
Align seg 1/1 to: PCT-US96-05611A-5 from: 1 to: 130
```

```
1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
26 ATGGCGTCTCAGAAACGTCCTCCAGCGTCACGGCTCCAAATACCTGCG 75
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
76 CACCGCCGACACCATGACATGCGCGTCATGCTTCTGCGCGCTCACG 125
34 rGAsp 35
|||||
126 GTGAC 130
```

```
seq_name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-6
seq_documentation_block:
; Sequence 6, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 2
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-05611A-6
```

```
alignment_scores:
Quality: 162.00      Length: 30
Ratio: 5.400         Gaps: 0
Percent Similarity: 100.000    Percent Identity: 100.000
```

```
alignment_block:
US-09-218-277-12 x PCT-US96-05611A-6/rev ..
```

```
Align seg 1/1 to reverse of: PCT-US96-05611A-6 from: 1 to: 129
```

```
30 LeuProArgHisArgAspThrGlyIleLeuAspSerIleGlyArgPheph 46
|||||
128 CTGCCGCGTCACCGTCGACACCGGCATCTGACTCCATCGCGCTCTT 79
46 eGlyGlyAspArgGlyAlaProLysArgGlySerGlyLys 59
|||||
78 CGGCGGTGACCGGTGTGCGCGAAGCTGGCTGTGGCAA 39
```

```
seq_name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-7
seq_documentation_block:
; Sequence 7, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
```

```

APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 3
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-7

alignment_scores:
Quality: 135.00 Length: 24
Ratio: 5.625 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-7 ..
Align seg 1/1 to: PCT-US96-05611A-7 from: 1 to: 133

59 LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuProG1 75
|||||
61 AAGAGCTCCACGACCGGCTGTACCGCGCATATGCTCCTGCCGCA 110
|||||
75 nlySerHisGlyArgThrGln 82
|||||
111 GAATCCGACGGCGGTACCCAG 132

seq_name: /sgnl_7/ptodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-10
seq_documentation_block:
; Sequence 10, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.

```

```

APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 6
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-05611A-10

alignment_scores:
Quality: 130.00 Length: 26
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-10/rev ..
Align seg 1/1 to reverse of: PCT-US96-05611A-10 from: 1 to: 111

146 AspaLagInGlyThrLeuSerIysIlePheLysLeuGlyArgAspse 162
|||||
110 GATGCCAGGCGACCTGTCCAAATTTCAAACTGCGCGCGGTGATAG 61
|||||
162 rArgSerGlySerProMetAlaArgArg 171
|||||
60 CCGTCTGGCTTCGCGATGCTAGAGCT 33

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2000, 19:34:34 ; Search time 12.55 Seconds

(Without alignments)
843.211 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171
Sequence: 1 MASQKRPSSGRHSKYLATAS.....SKIFKLGDRSGSGSPMARR 171

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR.64:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	66.1	197	1 MBHUB	myelin basic prote
2	76	44.4	171	1 MBGZB	myelin basic prote
3	46	26.9	128	1 MBRTS	myelin basic prote
4	46	26.9	167	2 A37246	myelin basic prote
5	45	26.3	328	1 MBMSB	goli1-myelin basic
6	41	24.0	169	1 MBBOB	myelin basic prote
7	41	24.0	171	1 MBPGB	myelin basic prote
8	14	8.2	14	2 S12904	protein kinase (EC
9	12	7.0	42	2 B92087	myelin basic prote
10	12	7.0	174	2 S08535	myelin basic prote
11	11	6.4	33	2 A60222	myelin basic prote
12	12	6.4	88	2 T43964	myelin basic prote
13	7	4.1	88	2 T44170	hypothetical prote
14	7	4.1	93	2 T09318	U24 [imported] - h
15	7	4.1	123	2 A69884	EoLF1 protein - hu
16	7	4.1	128	2 A60215	cell wall protein
17	7	4.1	155	2 B32989	myelin basic prote
18	7	4.1	155	2 T17889	myelin basic prote
19	7	4.1	259	2 T29727	glycine-rich prote
20	7	4.1	332	2 E70384	hypothetical prote
21	7	4.1	368	2 S64487	biotin synthetase
22	7	4.1	481	2 T56246	GTP-binding protei
23	7	4.1	508	1 NDBE33	lipopolysaccharide
24	7	4.1	529	2 A47131	exonuclease (EC 3.
25	7	4.1	532	2 T55389	Na+-dependent neut
26	7	4.1	532	2 T37188	neutral amino acid
27	7	4.1	545	2 T02279	neutral amino acid
28	7	4.1	565	2 T42593	hypothetical prote
29	7	4.1	573	2 S44605	exonuclease (EC 3. CO2F3.3 protein -

30	7	4.1	839	2 T39190
31	7	4.1	1151	2 T18535
32	7	4.1	1345	2 T41960
33	7	4.1	3305	2 T18358
34	6	3.5	60	2 A57413
35	6	3.5	88	2 S38267
36	6	3.5	96	2 G70117
37	6	3.5	102	2 S61055
38	6	3.5	109	2 B72213
39	6	3.5	113	2 S13494
40	6	3.5	115	2 A23925
41	6	3.5	116	2 S39434
42	6	3.5	116	2 S17567
43	6	3.5	124	2 S49957
44	6	3.5	125	2 S21419
45	6	3.5	132	2 T21416

ALIGNMENTS

RESULT 1
MBHUB
myelin basic protein - human
N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein p
.5K splice form
C:Species: Homo sapiens (man)
C>Date: 18-Dec-1981 #sequence, revision 25-Aug-1995 #text, change 22-Jun-1999
C:Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219;
R:Streicher, R.; Stoffel, W
Bio. Chem. Hoppe-Seyler 370, 503-510, 1989
A:Title: The organization of the human myelin basic protein gene. Comparison with the
A:Reference number: S10482; MUID:89302693
A:Accession: S10482
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-197 <STR>
A:Cross-references: EMBL:X17286; NID:q34490; PIDN:CMA35179.1; PID:e221974; PID:g11842
R:Kamholz, J.; De Ferra, F.; Puckett, C.; Lazzarini, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986
A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.
A:Reference number: A94106; MUID:86259714
A:Accession: A94106
A:Molecule type: mRNA
A:Residues: 1-59, 86-197 <KAM>
A:Cross-references: GB:M13577; NID:q187408; PIDN:AA59562.1; PID:g307160
A:Note: 18.5K splice form
A:Accession: B94106
A:Molecule type: mRNA
A:Residues: 1-197 <KA2>
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form
A:Note: a 17.2K splice form is also described
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K
R:Carnege, P.R.
Biochem. J. 123, 57-67, 1971
A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.
A:Reference number: A90256; MUID:72066400
A:Accession: A90256
A:Molecule type: protein
A:Residues: 2-59, 86-197 <CAR>
R:Proost, P.; Van Damme, J.; Opdenakker, G.
Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993
A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin b
A:Reference number: JH0802; MUID:93282820
A:Accession: JH0802
A:Molecule type: protein
A:Residues: 2-59, 86-197 <PRO>
A:Experimental source: Brain
R:Scoble, H.A.; Whitaker, J.N.; Biemann, K.
J. Neurochem. 47, 614-616, 1986
A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44
A:Reference number: A60862; MUID:86280476
A:Accession: A60862

A:Molecule type: protein
 A:Residues: 2-45,117-197 <SCO>
 A:Note: evidence for acetylated amino end
 R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Bleemann, K.
 J. Biol. Chem. 259, 5028-5031, 1984
 A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by mass spectrometry
 A:Reference number: A61420; MID:84185608
 A:Accession: A61420
 A:Molecule type: protein
 A:Residues: 46-59,86-116 <GIB>
 R:Wood, D.D.; Moscarello, M.A.
 J. Biol. Chem. 264, 5121-5127, 1989
 A:Title: The isolation, characterization, and lipid-aggregating properties of a citrullinized myelin basic protein peptide 46-59
 A:Reference number: A33273; MID:89174797
 A:Accession: A33273
 A:Molecule type: protein
 A:Residues: 15-25, 'X', 27-31, 'X', 33-59, 86-148, 'X', 150-156, 'X', 158-185, 'X', 187-196, 'X' <MC>
 A:Note: form C-8; residues designated 'X' were determined as citrulline
 R:Baldevin, G.S.; Carnegie, P.R.
 Biochem. J. 123, 69-74, 1971
 A:Title: Isolation and partial characterization of methylated arginines from the encephalic myelin basic protein
 A:Reference number: A90257; MID:72066401
 A:Contents: annotation; methylarginine
 A:Note: Arg-134 may be unmodified; monomethylarginine, or dimethylarginine in the approx 10% of the total
 R:Immon, V.A.; Wilks, A.V.; Carnegie, P.R.
 J. Immunol. 105, 1223-1230, 1971
 A:Reference number: A92806; MID:71088405
 A:Contents: annotation
 A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyelitis in mice
 R:Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prinsner, S.B.
 Genomics 6, 16-22, 1990
 A:Title: Repetitive DNA (TGCA)_n 5' to the human myelin basic protein gene: a new form of the myelin basic protein gene
 A:Reference number: I54219; MID:90152679
 A:Accession: I54219
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-59 <RES>
 A:Cross-references: GB:M63599; NID:q187402; PIDN:AAA59560.1; PID:q187403
 R:Roth, H.J.; Krongauz, K.E.; Keriolo de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.
 J. Neurosci. Res. 17, 321-328, 1987
 A:Title: Evidence for the expression of four myelin basic protein variants in the developing mouse brain
 A:Reference number: I56567; MID:87311781
 A:Accession: I56567
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-132,144-197 <RE2>
 A:Cross-references: GB:M30516; NID:q187410; PIDN:AAA59563.1; PID:q307161
 A:Accession: I73634
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-197 <RE3>
 A:Cross-references: GB:M30515; NID:q187412; PIDN:AAA59564.1; PID:q307162
 R:Roth, H.J.; Krongauz, K.; Preorius, P.J.; Crandall, B.F.; Campagnoni, A.T.
 J. Neurosci. Res. 16, 227-238, 1986
 A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3k myelin basic protein
 A:Reference number: I56565; MID:86308101
 A:Accession: I56565
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-59, 86-133, 145-197 <RE4>
 A:Cross-references: GB:M30047; NID:q187400; PIDN:AAA59559.1; PID:q307159
 R:Boulas, C.; Pang, H.; Mastromarino, F.; Moscarello, M.A.
 Arch. Biochem. Biophys. 322, 174-182, 1995
 A:Title: The isolation and characterization of four myelin basic proteins from the unbound myelin basic protein fraction
 A:Reference number: S66383; MID:96004793
 A:Accession: S66383
 A:Molecule type: protein
 A:Residues: 23-25, 'X', 27-39 <BOU>
 C:Comment: Four alternatively spliced forms of myelin basic protein have been observed, C:Genetics:
 A:Gene: GDB:MBP
 A:Cross-references: GDB:119379; OMIM:159430
 A:Map position: 18q22-18qter

A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
 C:Function:
 A:Description: probably helps maintain myelin structure
 C:Superfamily: myelin basic protein
 C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimmunity
 F:1-132,144-197/Product: myelin basic protein, 21.5k splice form #status predicted <MNT>
 F:2-132,144-197/Product: myelin basic protein, 20.2k splice form #status predicted <MNT>
 F:2-59,86-132,144-197/Product: myelin basic protein, 18.5k splice form #status predicted <MNT>
 F:2-59,86-132,144-197/Product: myelin basic protein, 17.2k splice form #status predicted <MNT>
 F:26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experimental
 F:134/Modified site: omega-N-methylarginine or omega-N-omega-N'-dimethylarginine (Arg)
 Query Match 66.1%; Score 113; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 2,36-112;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 59 KDSHNPARTAHYSGSLPQKSHGRTODENPVHFFKNTVPTPTPPSGKRGSLSRFSWG 118
 Db 85 KDSHNPARTAHYSGSLPQKSHGRTODENPVHFFKNTVPTPTPPSGKRGSLSRFSWG 144
 Oy 119 AEGORPFGYGGASPDYKSAHKGFGVDAGTSLKFKLGGHDSRSGSPMAR 171
 Db 145 AEGORPFGYGGASPDYKSAHKGFGVDAGTSLKFKLGGHDSRSGSPMAR 197
 RESULT 2
 MBP2B
 myelin basic protein - chimpanzee (tentative sequence)
 N:Alternate names: MBP
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 06-Sep-1996
 C:Accession: A03139
 R:Westall, F.C.; Thompson, M.; Kalter, S.S.
 Life Sci. 17, 219-223, 1975
 A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
 A:Reference number: A03139; MID:76009821
 A:Accession: A03139
 A:Molecule type: protein
 A:Residues: 1-171 <MES>
 C:Comment: This protein may function in maintaining the proper structure of myelin.
 C:Superfamily: myelin basic protein
 C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein
 F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
 F:107/Modified site: omega-N-methylarginine or omega-N-omega-N'-dimethylarginine (Arg)
 Query Match 44.4%; Score 76; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 4,46-73;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 ASQKRPDSQSHGSKYLTASTMDHARHGFPRHRDGIIDISIRFGGDCAPKRSRSGND 61
 Db 1 ASQKRPDSQSHGSKYLTASTMDHARHGFPRHRDGIIDISIRFGGDCAPKRSRSGND 60
 Oy 62 HHPARTAHYSGSLPQK 77
 Db 61 HHPARTAHYSGSLPQK 76
 RESULT 3
 MBP2S
 myelin basic protein S - rat
 N:Alternate names: small myelin basic protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Apr-1984 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
 C:Accession: B24351; A90275; A94243; A21062; A03142
 R:Schleich, M.; Budzinski, R.M.; Stoffel, W.
 Biol. Chem. Hoppe-Seyler 367, 825-834, 1986
 A:Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the proteolipid protein gene
 A:Reference number: B24351; MID:87026249
 A:Accession: B24351

A: Molecule type: mRNA
 A: Residues: 1-128 <SCH>
 A: Cross-references: EMBL:M25889; NID:g205321; PIDN:AAA1575.1; PID:g205322
 R: Dunkley, P.R.; Carnegie, P.R.
 Biochem. J. 141, 243-255, 1974
 A: Title: Amino acid sequence of the smaller basic protein from rat brain myelin.
 A: Reference number: A90275; MUID:75127355
 A: Accession: A90275
 A: Molecule type: protein
 A: Residues: 1-128 <DUN>
 A: Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in the
 R: McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKneally, S.; Shapiro, R.
 Science 179, 478-480, 1973
 A: Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogen
 A: Reference number: A94243; MUID:73180720
 A: Accession: A94243
 A: Molecule type: protein
 A: Residues: 46-86 <MCF>
 A: Note: the sequence reported for this encephalitogenic peptide differs from that shown
 R: Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.E.
 Cell 34, 799-806, 1983
 A: Title: Characterization of cloned cDNA representing rat myelin basic protein: absence
 A: Reference number: A21062; MUID:84026484
 A: Accession: A21062
 A: Molecule type: mRNA
 A: Residues: 1-124, 1, 126-128 <ROA>
 A: Experimental source: strain Sprague-Dawley
 C: Superfamily: myelin basic protein
 C: Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy
 F: 2-123/Product: myelin basic protein S #status experimental <MAT>
 F: 2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #statu
 F: 105/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg) (

Query Match 26.9%; Score 46; DB 1; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-41;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQKRPQSRHSGSKYLATASTMDARHGFLPRHDTGILDSIGRFF 46
 |||||||
 Db 1 MASQKRPQSRHSGSKYLATASTMDARHGFLPRHDTGILDSIGRFF 46

RESULT 4
 A37246
 myelin basic protein - guinea pig
 N: Alternate names: myelin A1 protein
 C: Species: Cavia porcellus (guinea pig)
 C: Date: 31-Jul-1991 #sequence, revision 31-Jul-1991 #text, change 07-Oct-1994
 C: Accession: A37246; C92087; A03140
 R: Delbier, G.E.; Martenson, R.E.; Krutzsch, H.C.; Kies, M.W.
 J. Neurochem. 43, 100-105, 1984
 A: Title: Sequence of guinea pig myelin basic protein.
 A: Reference number: A37246; MUID:84215086
 A: Accession: A37246
 A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 1-167 <DB1>
 R: Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971
 A: Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
 A: Reference number: A92087
 A: Accession: C92087
 A: Molecule type: protein
 A: Residues: 45-87 <SHA>
 C: Superfamily: myelin basic protein
 C: Keywords: myelin

Query Match 26.9%; Score 46; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-41;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRPQSRHSGSKYLATASTMDARHGFLPRHDTGILDSIGRFF 47
 |||||||
 Db 1 ASQKRPQSRHSGSKYLATASTMDARHGFLPRHDTGILDSIGRFF 46

RESULT 5
 MEMSB
 golli-myelin basic protein precursor - mouse
 N: Alternate names: golli-mbp protein; MBP
 N: Contains: myelin basic protein
 C: Species: Mus musculus (house mouse)
 C: Date: 17-Mar-1987 #sequence, revision 07-Oct-1994 #text, change 22-Jun-1999
 C: Accession: A45421; B45421; A90875; A90867; A26591; B26591; A60920; I48407; I58996;
 R: Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kamp, K.; Amur-Umarjee, S.; Land
 J. Biol. Chem. 268, 4930-4938, 1993
 A: Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene tha
 A: Reference number: A45421; MUID:93186801
 A: Accession: A45421
 A: Molecule type: mRNA
 A: Residues: 1-190; 217-276; 316-328 <CAM1>
 A: Cross-references: GB:107507; NID:g193584
 A: Experimental source: clone J37
 A: Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified
 A: Accession: B45421
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-191, 'SSEP' <CAM2>
 A: Cross-references: GB:107508; NID:g193586; PIDN:AAA37721.1; PID:g193587
 A: Experimental source: clone Bg21
 A: Note: sequence extracted from NCBI backbone (NCBIN:126700; NCBI:126715)
 R: de Ferris, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Mollineaux, S.; Lazzar
 Cell 43, 721-727, 1985
 A: Title: Alternative splicing accounts for the four forms of myelin basic protein.
 A: Reference number: A90875; MUID:86079355
 A: Accession: A90875
 A: Molecule type: mRNA
 A: Residues: 134-328 <DEF>
 A: Cross-references: GB:M1004; GB:M1169; NID:g199060; PIDN:AAA39502.1; PID:g387419
 R: Takahashi, N.; Roach, A.; Teplow, D.B.; Prusiner, S.B.; Hood, L.
 Cell 42, 139-148, 1985
 A: Title: Cloning and characterization of the myelin basic protein gene from mouse: on
 A: Reference number: A90867; MUID:85254913
 A: Accession: A90867
 A: Molecule type: DNA
 A: Residues: 134-190; 217-328 <TA>
 A: Cross-references: GB:M11533; NID:g199044; PIDN:AAA39496.1; PID:g387414
 A: Experimental source: 18.5K
 R: Newman, S.; Kitamura, K.; Campagnoni, A.T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987
 A: Title: Identification of a cDNA coding for a fifth form of myelin basic protein in
 A: Reference number: A94188; MUID:87118269
 A: Accession: A26591
 A: Molecule type: mRNA
 A: Residues: 134-274; 316-328 <NEW1>
 A: Cross-references: GB:M15060; NID:g199048; PIDN:AAA59711.1; PID:g199049
 A: Experimental source: clone M722; splice form 17.22K
 A: Accession: B26591
 A: Molecule type: mRNA
 A: Residues: 134-190; 217-263; 275-328 <NEW2>
 A: Cross-references: GB:M15062; NID:g199050
 A: Experimental source: clone M78; splice form 17.24K
 R: Kitamura, K.; Newman, S.U.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V
 J. Neurochem. 54, 2032-2041, 1990
 A: Title: Expression of a novel transcript of the myelin basic protein gene.
 A: Reference number: A60920; MUID:90250449
 A: Accession: A60920
 A: Status: translation not shown
 A: Molecule type: mRNA
 A: Residues: 134-190; 217-274; 316-328 <KIT>
 A: Experimental source: M41; splice form 14K

R:Grlma, B.; Zelenika, D.; Pessac, B.
 J. Neurochem. 59, 2318-2323, 1992
 A>Title: A novel transcript overlapping the myelin basic protein gene.
 A:Reference number: 148407; MUID:93057537
 A:Accession: 148407
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-191, 'SSEP' <GR1>
 A:Cross-references: EMBL:X67319; NID:951332; PIDN:CA47733.1; PID:951333
 A:Note: submitted to the EMBL Data Library, July 1992
 R:Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
 A>Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin bas
 A:Reference number: 158996; MUID:84119431
 A:Accession: 158996
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 219-248 <ZEL>
 A:Cross-references: GB:X00989; NID:9199037; PIDN:AA39495.1; PID:9554195
 R:Miura, M.; Tamura, T.
 Gene 75, 31-38, 1989
 A>Title: The promoter elements of the mouse myelin basic protein gene function efficient
 A:Reference number: 154033; MUID:89252919
 A:Accession: 154033
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 134-157 <MTU>
 A:Cross-references: GB:M24410; NID:9199052; PIDN:AA39498.1; PID:9554196
 R:Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.
 EMBO J. 7, 77-83, 1988
 A>Title: Gene organization and transcription of duplicated MBP genes of myelin deficient
 A:Reference number: 153256; MUID:88196094
 A:Accession: 153256
 A>Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 217-229, 'NH', 232-250 <OKA>
 A:Cross-references: GB:M36275; NID:9199069; PIDN:AA39504.1; PID:9293725
 A:Note: hypothetical translation of the reversed and complementary sequence to that show
 C:Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.2K, 17.2K and
 C:Genetics:
 A:Gene: Goll1-mbp; sh1-mld
 A:Introns: 190/3; 250/3; 262/3; 273/3; 314/3
 C:Function:
 A:Description: probably helps maintain myelin structure
 C:Superfamily: myelin basic protein
 C:Keywords: alternative splicing; myelin; structural protein
 F:1-190, 217-276, 316-328/Product: Goll1-mbp protein (clone J37) #status predicted <MA1>
 F:134-328/Product: myelin basic protein, splice form 21.5K #status predicted <MA1>
 F:134-274, 316-328/Product: myelin basic protein, splice form 17K-a #status predicted <MA
 F:134-190, 217-328/Product: myelin basic protein, splice form 18.5K #status predicted <MA
 F:134-190, 217-263, 275-328/Product: myelin basic protein, splice form 17K-b #status predi
 F:134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predict

Query Match 26.3%; Score 45; DB 1; Length 328;
 Best Local Similarity 100.0%; Pred. No. 7e-40;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 HGRTPDNPVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 122
 DB 234 HGRTPDNPVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 278

RESULT 6
 MBOB
 myelin basic protein - bovine
 N:Alternate names: myelin AI protein
 N:Contains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 18-Dec-1981 #sequence revision 18-Dec-1981 #text change 07-May-1999
 C:Accession: A92089; A92160; A92087; S54343; A61641; B61641; A03140
 R:Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.
 J. Biol. Chem. 246, 5770-5784, 1971

A>Title: Basic AI protein of the myelin membrane. The complete amino acid sequence.
 A:Reference number: A92089; MUID:72007306
 A:Accession: A92089
 A:Molecule type: protein
 A:Residues: 1/'S', 2-169 <EYL>
 R:Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
 J. Biol. Chem. 249, 559-567, 1974
 A>Title: Specific cleavage of the AI protein from myelin with cathepsin D.
 A:Reference number: A92160; MUID:74070688
 A:Accession: A92160
 A:Molecule type: protein
 A:Residues: 1-169

 R:Shapira, R.; McKenally, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971
 A>Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bo
 A:Reference number: A92087
 A:Accession: A92087
 A:Molecule type: protein
 A:Residues: 43-87 <SHA>
 R:Okazaki, K.; Obata, N.R.; Inoue, S.; Hidaka, H.
 Biochem. J. 306, 551-555, 1995
 A>Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in g
 A:Reference number: S54343; MUID:95194333
 A:Accession: S54343
 A:Molecule type: protein
 A:Residues: 74-75, 'HG', 78-82, 'D', 84-88, 105, 'X', 107-108, 'X', 110-114, 'X', 116-119 <OKA>
 R:Takamatsu, K.; Tatemoto, K.
 Neurochem. Res. 17, 239-246, 1992
 A>Title: Isolation and characterization of two novel peptide amides originating from
 A:Reference number: A61641; MUID:92319189
 A:Accession: A61641
 A:Molecule type: protein
 A:Residues: 1-12 <TAK>
 A:Accession: B61641
 A:Molecule type: protein
 A:Residues: 1-16 <RA2>
 A:Note: these peptides have carboxyl-terminal amides probably produced by a non-enzym
 R:Brostoff, S.; Eylar, E.H.
 Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971
 A>Title: Localization of methylated arginine in the AI protein from myelin.
 A:Reference number: A93777; MUID:71153946
 A:Contents: annotation
 A:Note: Arg-106 is modified to monomethylarginine and dimethylarginine
 R:Eylar, E.H.; Caccam, J.; Jackson, J.C.; Westall, F.C.; Robinson, A.B.
 Science 168, 1220-1223, 1970
 A>Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site
 A:Reference number: A94241; MUID:70176977
 A:Contents: annotation
 A:Note: the region including residues 114-122 induces experimental allergic encephalo
 C:Superfamily: myelin basic protein
 C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune ence
 F:1-169/Product: myelin basic protein #status experimental <MA1>
 F:1-16/Product: myelin peptide amide-16 #status experimental <PA16>
 F:1-12/Product: myelin peptide amide-12 #status experimental <PA12>
 F:1/Modified site: acetylated amino end (Ala) #status experimental
 F:12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide
 F:16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide
 F:106/Modified site: omega-N-methylarginine or omega-N-methylarginine (Arg

Query Match 24.0%; Score 41; DB 1; Length 169;
 Best Local Similarity 100.0%; Pred. No. 7.2e-36;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 QDENPVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 122
 DB 80 QDENPVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 120

RESULT 7
 MBPG
 myelin basic protein - pig (tentative sequence)
 N:Alternate names: myelin AI protein

N:Contains: myelin basic protein amide 14
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 07-May-1999
C:Accession: A61640; A36245
R:Kira, J.; Delbier, G.E.; Kruttsch, H.C.; Martenson, R.E.
J. Neurochem. 44, 134-142, 1985
A:Title: Amino acid sequence of porcine myelin basic protein.
A:Reference number: A61640; MUID:85036964
A:Accession: A61640
A:Molecule type: protein
A:Residues: 1-171 <KIR>
A:Note: some peptides were ordered by homology
R:Takamatsu, K.; Tatemoto, K.
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.
A:Reference number: A36245; MUID:91058553
A:Accession: A36245
A:Molecule type: protein
A:Residues: 1-14 <TRK>
A:Note: the sequence in the abstract is inconsistent with that in figure 3 in having Glu
A:Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic
C:Superfamily: myelin basic protein
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune enceph
F:1-171/Product: myelin basic protein #status experimental <MAT>
F:1-14/Product: myelin peptide amide-14 #status experimental <PAL2>
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:1/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide am
F:107/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg) (

Query Match 24.0%; Score 41; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.3e-36;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 QDENPVVHFKNIVTPRPPSGKRGSLSRFSWGAEGQ 122
DB 81 QDENPVVHFKNIVTPRPPSGKRGSLSRFSWGAEGQ 121

RESULT 8
S12904
Protein kinase (EC 2.7.1.37) - starfish (Plaster ochraceus)
C:Species: Plaster ochraceus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C:Accession: S12904
R:Sanquerra, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by
A:Reference number: S12904; MUID:91032186
A:Accession: S12904
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SAN>
C:Keywords: phosphotransferase

Query Match 8.2%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 NIVTPRPPPSQGR 106
DB 1 NIVTPRPPPSQGR 14

RESULT 9
B92087
myelin basic protein - rabbit (fragment)
N:Alternate names: myelin A1 protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Sep-1993
C:Accession: B92087; A03140
R:Shapira, R.; McKeenly, S.S.; Chou, F.; Kibler, R.F.

J. Biol. Chem. 246, 4630-4640, 1971
A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bo
A:Reference number: A92087
A:Accession: B92087
A:Molecule type: protein
A:Residues: 1-42 <SRH>
C:Superfamily: myelin basic protein
C:Keywords: myelin

Query Match 7.0%; Score 12; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 DRGAPKRGSGKD 60
DB 4 DRGAPKRGSGKD 15

RESULT 10
S08535
myelin basic protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 13-Aug-1999
C:Accession: S08535
R:Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D.
Glia 2, 241-249, 1989
A:Title: Developmental accumulation and heterogeneity of myelin basic protein transcr
A:Reference number: S08535; MUID:89358239
A:Accession: S08535
A:Molecule type: mRNA
A:Residues: 1-174 <ZOP>
A:Cross-references: EMBL:X17103; NID:963594; PIDN:CAA34959.1; PID:963595
C:Superfamily: myelin basic protein

Query Match 7.0%; Score 12; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 148 QGTLSKIFKLG 159
DB 147 QGTLSKIFKLG 158

RESULT 11
A60222
myelin basic protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 17-Jul-1994
C:Accession: A60222
R:Aruga, J.; Okano, H.; Mikoshiba, K.
J. Neurochem. 56, 1222-1226, 1991
A:Title: Identification of the new isoforms of mouse myelin basic protein: the existe
A:Reference number: A60222; MUID:91162193
A:Accession: A60222
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-33 <ARU>

Query Match 6.4%; Score 11; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 GRGLSRFSW 117
DB 23 GRGLSRFSW 33

RESULT 12
T43984
hypothetical protein U24 [Imported] - human herpesvirus 6 (strain HST)

C:Species: human herpesvirus 6
A:Variety: strain HST
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43984
R: Iseigawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Reference number: Z22732
A:Accession: T43984
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-88 <ISE>
A:Cross-references: EMBL:AB021506; PIDN:BA078245.1
A:Experimental source: strain HST; pop. variant B
C:Genetics:
A:Note: U24

Query Match 4.1%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 PRTPPS 103
|||||
DB 4 PRTPPS 10

RESULT 13
U24 [Imported] - human herpesvirus 6 (strain Z29)
C:Species: human herpesvirus 6
A:Variety: strain Z29
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44170
R: Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A:Reference number: Z22734; MUID:99412318
A:Accession: T44170
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-88 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AD049637.1
A:Experimental source: strain Z29; variant B
C:Genetics:
A:Note: U24

Query Match 4.1%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 PRTPPS 103
|||||
DB 4 PRTPPS 10

RESULT 14
T09318
EoLF1 protein - human herpesvirus 6 (strain U1102)
C:Species: human herpesvirus 6
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T09318
R: Nicholas, J.; Martin, M.
J. Virol. 68, 597-610, 1994
A:Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hu
A:Reference number: Z16644; MUID:94118404
A:Accession: T09318
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-93 <NIC>
A:Cross-references: EMBL:L25528; NID:g451932; PID:g451949
C:Genetics:

A:Gene: EoLF1

Query Match 4.1%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 PRTPPS 103
|||||
DB 10 PRTPPS 16

RESULT 15
A69884
cell wall protein homolog ymag - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: A69884
R: Kunst, F.; Ogatawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Boulanger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gal
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardio
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchida
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033
A:Accession: A69884
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-123 <KUN>
A:Cross-references: GB:Z09113; GB:AL009126; NID:g2634090; PIDN:CAB13615.1; PID:el1833
A:Experimental source: strain 168
C:Genetics:
A:Gene: ymag

Query Match 4.1%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 RPFGRG 129
|||||
DB 71 RPFGRG 77

Search completed: September 26, 2000, 19:37:20
Job time: 166 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:36:23 ; Search time 7.44 Seconds.

(without alignments)
712.250 Million cell updates/sec

Title: US-09-218-277-12

Sequence: 1 MASQKRPGRHSGSKYLATAS.....SKIFKLGDRSGSGPMARR 171

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 85661 seqs, 30989116 residues

Word size: 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	66.1	196	1 MBP_HUMAN	P02686 homo sapien
2	75	44.4	171	1 MBP_PANTR	P06906 pan troglod
3	46	26.9	167	1 MBP_CAVPO	P25188 cavia porce
4	45	26.3	127	1 MBP_RAT	P02688 rattus norv
5	45	26.3	194	1 MBP_MOUSE	P04370 mus musculu
6	41	24.0	169	1 MBP_BOVIN	P02687 bos taurus
7	41	24.0	171	1 MBP_PIG	P01558 sus scrofa
8	12	7.0	42	1 MBP_RABIT	P25274 oryctolagus
9	12	7.0	173	1 MBP_CHICK	P15720 gallus gall
10	8	4.7	154	1 MBP_RAUER	Q91325 raja erinac
11	8	4.7	154	1 MBP_SQUAC	Q91435 squallus aca
12	8	4.7	323	1 PCP3_AMPCA	P00483 amphidinlum
13	7	4.1	154	1 MBP_HETFR	P20939 heterodontu
14	7	4.1	368	1 YG3V_YEAST	P53295 saccharomyc
15	7	4.1	481	1 LBP_BAT	Q63313 rattus norv
16	7	4.1	508	1 EXON_HSVB	P28919 equine herp
17	7	4.1	532	1 SAT1_HUMAN	P43007 homo sapien
18	7	4.1	573	1 YK3_CAEEL	P42480 caenorhabd1
19	7	4.1	1345	1 VCAP_HSV7J	P52347 herpes simp
20	7	4.1	3305	1 APLP_MANSE	Q25490 manduca sex
21	6	3.5	88	1 CUV70_LOCHI	P60233 locusta mig
22	6	3.5	112	1 H34_STYLE	P61198 stylynychia
23	6	3.5	112	1 OLF9_MOUSE	Q60885 mus musculu
24	6	3.5	116	1 AON3_PIG	P40420 sus scrofa
25	6	3.5	124	1 YIC5_YEAST	P40542 saccharomyc
26	6	3.5	134	1 YNBL_SYND7	P35086 synchococc
27	6	3.5	148	1 KOR1_HSVB	Q08104 bovine herp
28	6	3.5	150	1 EXON_PRVN3	P30660 pseudoribla
29	6	3.5	155	1 YKFB_ECOLI	P77166 escherichia
30	6	3.5	156	1 RR7_MAIZE	P12333 zea mays (m
31	6	3.5	156	1 R77_ORYSA	P15423 oryza sativ
32	6	3.5	184	1 TRIS_RABIT	P02645 oryctolagus
33	6	3.5	185	1 PHNN_ECOLI	P16690 escherichia

ALIGNMENTS

RESULT 1	ID	MBP_HUMAN	STANDARD;	PRT;	196 AA.
AC	P02686;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	15-FEB-2000 (Rel. 39, Last annotation update)				
DE	MYELIN BASIC PROTEIN (MBP).				
GN	MBP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
NC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE; 89302693.				
RA	Streicher R., Stoffel W.;				
RT	"The organization of the human myelin basic protein gene. Comparison				
RT	with the mouse gene.";				
RL	Biol. Chem. Hoppe-Seyler 370:503-510(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE; 87311781.				
RA	Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F.,				
RA	Campanoni A.T.;				
RT	"Isolation and characterization of a cDNA coding for a novel human				
RT	17.3k myelin basic protein (MBP) variant.";				
RL	J. Neurosci. Res. 16:227-238(1986).				
RN	[4]				
RP	SEQUENCE OF 1-58 AND 85-196 FROM N.A.				
RA	MEDLINE; 86259714.				
RA	Kambholz J., de Ferreira F., Puckett C., Lazzarini R.A.;				
RT	"Identification of three forms of human myelin basic protein by cDNA				
RT	cloning.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).				
RN	[5]				
RP	SEQUENCE OF 1-58 AND 85-196.				
RA	MEDLINE; 72066400.				
RA	Carnegele P.R.;				
RT	"Amino acid sequence of the encephalitogenic basic protein from human				
RT	myelin.";				
RL	Biochem. J. 123:57-67(1971).				
RN	[6]				
RP	SEQUENCE OF 45-58 AND 85-114, AND REVISIONS.				
RA	Shapira R., McKeenally S.S., Chou F., Kibler R.F.;				
RT	"Encephalitogenic fragment of myelin basic protein. Amino acid				
RT	sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";				
RL	J. Biol. Chem. 246:4630-4640(1971).				
RN	[7]				

34	6	3.5	186	1	TRIS_HUMAN	P19277 homo sapien
35	6	3.5	186	1	TRIS_RAT	P13413 rattus norv
36	6	3.5	206	1	ALAI_MOUSE	Q63805 mus musculu
37	6	3.5	214	1	DCOP_THDAC	Q74110 thermoplasm
38	6	3.5	217	1	UNG_PSEDE	P29950 pseudomonas
39	6	3.5	225	1	Y638_MENJA	Q58055 methanococc
40	6	3.5	244	1	FNRA_PSEST	P47200 pseudomonas
41	6	3.5	249	1	YBFT_BACSU	Q31458 bacillus su
42	6	3.5	249	1	YDD1_SCHPO	Q10426 schizosacch
43	6	3.5	251	1	TPIS_COPCI	Q12574 coprinus c1
44	6	3.5	251	1	YAT8_SCHPO	Q10153 schizosacch
45	6	3.5	253	1	CHIO_TOBAC	P17514 nicotiana t

RP SEQUENCE OF 1-58 FROM N.A.
 RX MEDLINE: 90152679.
 RA Boylan K.B., Ayres T.M., Popko B., Takahashi N., Hood L.E.,
 RA Prusiner S.B.;
 RT "Repetitive DNA (7GGA)n 5' to the human myelin basic protein gene: a
 RT new form of oligonucleotide repetitive sequence showing length
 RT polymorphism".
 RL Genomics 6:16-22(1990).
 RN [8]
 RP METHYLATION.
 RX MEDLINE: 72066401.
 RA Baldwin G.S., Carnegie P.R.;
 RT "Isolation and partial characterization of methylated arginines from
 RT the encephalitogenic basic protein of myelin".
 RL Biochem. J. 123:69-74(1971).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS: 21.5 KDA (SHOWN HERE), 18.5
 CC KDA (THE MOST ABUNDANT) AND 17.2 KDA; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
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 CC -----
 DR EMBL: M15577; AAA59562.1; -
 DR EMBL: M30516; AAA59563.1; -
 DR EMBL: M30515; AAA59564.1; -
 DR EMBL: M30047; AAA59559.1; -
 DR EMBL: X17286; CAA35179.1; -
 DR EMBL: X17287; CAA35179.1; JOINED.
 DR EMBL: X17280; CAA35179.1; JOINED.
 DR EMBL: X17288; CAA35179.1; JOINED.
 DR EMBL: X17369; CAA35179.1; JOINED.
 DR EMBL: X17289; CAA35179.1; JOINED.
 DR EMBL: M63599; AAA59560.1; -
 DR PIR: A24153; MBHUB.
 DR PIR: S10482; S10482.
 DR MIM: 159430; -
 DR PFM: 159430; Myelin_MBP, 1.
 DR PRINTS: PRO0212; MYELINMBP.
 DR PROSITE: PS00569; MYELIN_MBP, 1.
 KW Myelin; structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 FT INT_MET 0 0
 FT MOD_RES 1 133 ACETYLATION.
 FT MOD_RES 133 133 METHYLATION (MONO-16% OR DI-160%).
 FT DOMAIN 45 114 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS IN MONKEYS, RABBITS,
 FT AND RATS BUT NOT IN GUINEA PIGS.
 FT DOMAIN 138 148 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS.
 FT VARSPLIC 59 84 MISSING (IN 18.5 KDA ISOFORM AND 17.2 KDA
 FT ISOFORM).
 FT VARSPLIC 132 142 MISSING (IN 17.2 KDA ISOFORM).
 FT SEQUENCE 196 AA; 21362 MW; 23EBD0C1CE689653 CRC64;

Query Match 66.1%; Score 113; DB 1; Length 196;
 Best Local Similarity 100.0%; Pred. No. 2.6e-111;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 KDSHNPARTAHYGSLSPPKSHGRTQDENPVVHFPEKNTVTPPTPPSGKRGSLSPFSSWG 118
 DB 84 KDSHNPARTAHYGSLSPPKSHGRTQDENPVVHFPEKNTVTPPTPPSGKRGSLSPFSSWG 143
 OY 119 ASGQRGFGYGGASDYKSAHKGFKGVDAQGLTSLFKLGGRDSGSPMAR 171

DB 144 ASGQRGFGYGGASDYKSAHKGFKGVDAQGLTSLFKLGGRDSGSPMAR 196
 RESULT 2
 MBP_PANTR
 ID MBP_PANTR STANDARD; PRT; 171 AA.
 AC P06506;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 RN [1]
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE: 76009821.
 RA Westall F.C., Thompson M., Kalter S.S.;
 RT "The proposed sequence of the encephalitogenic protein from
 RT chimpanzee brain."
 RL Life Sci. 17:219-223(1975).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC PIR: A03139; MEC2B.
 DR PFM: PF01669; Myelin_MBP, 1.
 DR PRINTS: PRO0212; MYELINMBP.
 DR PROSITE: PS00569; MYELIN_MBP, 1.
 KW Myelin; structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis.
 FT MOD_RES 1 107 METHYLATION (BY SIMILARITY).
 FT MOD_RES 107 107 ACETYLATION.
 FT SEQUENCE 171 AA; 18560 MW; E9FED59D6933293 CRC64;

Query Match 44.4%; Score 76; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASQKRPDSQHGSKYLTATSTMDHARHGFPRHRDGIIDSGRFGGGRGAPKRSKGDS 61
 DB 1 ASQKRPDSQHGSKYLTATSTMDHARHGFPRHRDGIIDSGRFGGGRGAPKRSKGDS 60
 OY 62 HNPARTAHYGSLSPPKSHGRTQDENPVVHFPEKNTVTPPTPPSGKRGSLSPFSSWG 118
 DB 61 HNPARTAHYGSLSPPKSHGRTQDENPVVHFPEKNTVTPPTPPSGKRGSLSPFSSWG 143

RESULT 3
 MBP_CAVPO
 ID MBP_CAVPO STANDARD; PRT; 167 AA.
 AC P25188;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN Cavia porcellus (Guinea pig).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 84215086.
 RA Delbier G.E., Mattenson R.E., Krutzsch H.C., Kies M.W.;
 RT "Sequence of guinea pig myelin basic protein."
 RL J. Neurochem. 43:100-105(1984).
 RN [2]
 RP SEQUENCE OF 45-87.
 RA Shapira R., McKenally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments."

```

CC CC SMALLER ONE. SHOWN HERE, IS MISSING 40 RESIDUES (FOLLOWING RESIDUE
CC 113 OR 114) WITH RESPECT TO THE LARGER ONES FROM OTHER SPECIES.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
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CC -----
CC DR EMBL; M25889; AAA41575.1; "-
CC EMBL; K00512; "- NOT_ANNOTATED_CDS.
CC DR PIR; A03142; MBRTS.
CC DR PIR; B24351; B24351.
CC DR PIR; A21062; A21062.
CC DR PIR; PFO1669; Myelin_MBP; 1.
CC DR PRINTS; PRO0212; MYELINMB.
CC DR PROSITE; PS00569; MYELINMBP; 1.
CC KW Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;
CC Autoimmune encephalomyelitis; Alternative splicing.
CC FT INIT_MET 0
CC FT MOD_RES 1
CC FT MOD_RES 104 ACETYLATION.
CC FT CONFLICT 46 METHYLATION (MONO-:44% OR DI-:11%).
CC FT CONFLICT 47 SG -> GS (IN REF. 4).
CC FT CONFLICT 124 M -> I (IN REF. 2).
CC FT SEQUENCE 127 AA; 14080 MW; B4C9F33C19A9E137 CRC64;
CC -----
QY 2 ASQKRPQGRHGSKYLTASTMDHARHGFLPRHRDPTGLDLSIGREF 46
QY |||||||
DB 1 ASQKRPQGRHGSKYLTASTMDHARHGFLPRHRDPTGLDLSIGREF 45
DB |||||||
DB 1 ASQKRPQGRHGSKYLTASTMDHARHGFLPRHRDPTGLDLSIGREF 45
DB |||||||

RESULT 5
MBP_MOUSE STANDARD; PRT; 194 AA.
AC P04370:
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP).
DE MBP.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN [1]
NC SEQUENCE FROM N.A. (ALL FOUR FORMS).
RP RP MEDLINE; 86079555.
RA de Ferra F., Engh H., Hudson L., Kamholz J., Puckett C., Molineaux S.,
RA Lazzarini R.A.,
RA "Alternative splicing accounts for the four forms of myelin basic
RA protein."
RA Cell 43:721-727(1985).
RL [2]
RP RP SEQUENCE FROM N.A. (18.5 KDA FORM).
RP RP MEDLINE; 85254913.
RA Takahashi N., Roach A., Teplow D.B., Fustlier S.B., Hood L.;
RA "Cloning and characterization of the myelin basic protein gene from
RA mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate
RA use of exons."
RA Cell 42:139-148(1985).
RL [3]
RP RP SEQUENCE FROM N.A. (17 KDA FORM).
RP RP MEDLINE; 87118269.
RA Newman S., Kitamura K., Campagnoni A.T.;
RA "Identification of a cDNA coding for a fifth form of myelin basic
RA protein in mouse."

```

RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).
 RN [4]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE: 89252919.
 RA Mura M., Tamura T.A., Aoyama A., Mikhosha K.;
 RT "The promoter elements of the mouse myelin basic protein gene
 function efficiently in NG108-15 neuronal/gliai cells.";
 RT Gene 75:31-38(1989).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- ALTERNATIVE PRODUCTS: FOUR ISOFORMS: 21.5 KDA (SHOWN HERE), 18.5
 CC KDA, 17 KDA AND 14 KDA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
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 CC -----
 DR EMBL: M11533: AAA39496.1: -
 DR EMBL: M11291: AAA39496.1: JOINED.
 DR EMBL: M11528: AAA39496.1: JOINED.
 DR EMBL: M11530: AAA39496.1: JOINED.
 DR EMBL: M11531: AAA39496.1: JOINED.
 DR EMBL: M11532: AAA39496.1: JOINED.
 DR EMBL: M11533: AAA39496.1: JOINED.
 DR EMBL: M11291: AAA39497.1: JOINED.
 DR EMBL: M11528: AAA39497.1: JOINED.
 DR EMBL: M11530: AAA39497.1: JOINED.
 DR EMBL: M11531: AAA39497.1: JOINED.
 DR EMBL: M11532: AAA39497.1: JOINED.
 DR EMBL: M11533: AAA39497.1: JOINED.
 DR EMBL: L00398: AAA39499.1: JOINED.
 DR EMBL: L00400: AAA39499.1: JOINED.
 DR EMBL: L00401: AAA39499.1: JOINED.
 DR EMBL: L00402: AAA39499.1: JOINED.
 DR EMBL: L00403: AAA39499.1: JOINED.
 DR EMBL: L00404: AAA39500.1: JOINED.
 DR EMBL: L00405: AAA39500.1: JOINED.
 DR EMBL: L00398: AAA39500.1: JOINED.
 DR EMBL: L00399: AAA39500.1: JOINED.
 DR EMBL: L00400: AAA39500.1: JOINED.
 DR EMBL: L00401: AAA39500.1: JOINED.
 DR EMBL: L00402: AAA39500.1: JOINED.
 DR EMBL: L00403: AAA39500.1: JOINED.
 DR EMBL: L00404: AAA39500.1: JOINED.
 DR EMBL: L00405: AAA39500.1: JOINED.
 DR EMBL: L00398: AAA39502.1: JOINED.
 DR EMBL: L00399: AAA39502.1: JOINED.
 DR EMBL: L00400: AAA39502.1: JOINED.
 DR EMBL: L00401: AAA39502.1: JOINED.
 DR EMBL: L00402: AAA39502.1: JOINED.
 DR EMBL: L00403: AAA39502.1: JOINED.
 DR EMBL: L00404: AAA39502.1: JOINED.
 DR EMBL: L00405: AAA39502.1: JOINED.
 DR EMBL: M24410: AAA39498.1: -
 DR PIR: A24772: MEMSB.
 DR PIR: A26591: A26591.
 DR PIR: B26591: B26591.
 DR MGD: MGI:96925: MBP.
 DR PFAM: PF01669: Myelin_MBP. 1.
 DR PRINTS: PRO0212: MYELINMBP.
 DR PROSITE: PS00569: MYELIN_MBP. 1.
 DR Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 FT INIT_MET 0 0
 FT MOD_RES 1 130 ACETYLATION (BY SIMILARITY).
 FT VARSPIC 57 82 METHYLATION (BY SIMILARITY).
 FT MISSING (IN 18.5 KDA ISOFORM AND 14 KDA

FT VARSPIC 140 180 ISOFORM).
 FT MISSING (IN 17 KDA ISOFORM AND 14 KDA
 FT ISOFORM).
 SQ SEQUENCE 194 AA: 21371 MW; D208CACOCF52ACD2 CRC64;
 Query Match 26.3%; Score 45; DB 1; Length 194;
 Best Local Similarity 100.0%; Pred. No. 7,4e-40;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 78 HGRTPDENVVHFKNIVTPRTPPSGRGSLSRFSWGAEGQ 122
 Db 100 HGRTPDENVVHFKNIVTPRTPPSGRGSLSRFSWGAEGQ 144
 RESULT 6
 ID MBP_BOVIN STANDARD; PRT; 169 AA.
 AC P02687;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP) (MYELIN A1 PROTEIN).
 GN MBP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 72007306.
 RA Eylar E.H., Brostoff S.W., Hashin G., Caccam J., Burnett P.;
 RT "Basic A1 protein of the myelin membrane. The complete amino acid
 RT sequence.";
 RL J. Biol. Chem. 246:5770-5784(1971).
 RN [2]
 RP REVISION.
 RX MEDLINE: 74070688.
 RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";
 RL J. Biol. Chem. 249:559-567(1974).
 RN [3]
 RP SEQUENCE OF 43-87.
 RA Shapira R., McKneally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640(1971).
 RN [4]
 RP METHYLATION.
 RX MEDLINE: 71153946.
 RA Brostoff S.W., Eylar E.H.;
 RT "Localization of methylated arginine in the A1 protein from myelin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).
 RN [5]
 RP SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.
 RX MEDLINE: 70178977.
 RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;
 RT "Experimental allergic encephalomyelitis: synthesis of
 RT disease-inducing site of the basic protein.";
 RL Science 168:1220-1223(1970).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC PIR: A03140: MBP.
 DR PFAM: PF01669: Myelin_MBP. 1.
 DR PRINTS: PRO0212: MYELINMBP.
 DR PROSITE: PS00569: MYELIN_MBP. 1.
 DR Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis.
 FT INIT_MET 0 0
 FT MOD_RES 1 106 ACETYLATION.
 FT VARSPIC 114 122 METHYLATION (MONO- OR DI-).
 FT INDUCES EXPERIMENTAL AUTOIMMUNE

FT SEQUENCE 169 AA: 18323 MW: 8E1157B7A1978484 CRC64: ENCEPHALOMYELITIS

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 169;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 ODENVVHFFKNIVTPRPPPSQGRGLSLRFSWGAEQ 122
DB 80 ODENVVHFFKNIVTPRPPPSQGRGLSLRFSWGAEQ 120

RESULT 7
MBP_PIG ID MBP_PIG STANDARD: PRT; 171 AA.

AC P81558;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP).
GN MBP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE.
RC TISSUE-BRAIN;
RX MEDLINE; 85056964.
RA Ira J. -, Delbler G. E., Krutzsch H. C., Martenson R. E.;
RT "Amino acid sequence of porcine myelin basic protein.";
RL J. Neurochem. 44:134-142(1985).
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KM Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
KW Autoimmune encephalomyelitis.
FT MOD_RES 1 1
FT MOD_RES 107 107 METHYLATION (MONO- OR DI-) (BY SIMILARITY)
FT DOMAIN 115 123 INDUCES EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS (BY SIMILARITY).
FT SEQUENCE 171 AA: 18487 MW: 287AEDF2F24028D9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 171;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 ODENVVHFFKNIVTPRPPPSQGRGLSLRFSWGAEQ 122
DB 81 ODENVVHFFKNIVTPRPPPSQGRGLSLRFSWGAEQ 121

RESULT 8
MBP_RABIT ID MBP_RABIT STANDARD: PRT; 42 AA.

AC P25274;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP) (MYELIN AL PROTEIN) (FRAGMENT).
GN MBP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RA Shastra R., McNeally S. S., Chou F., Kibler R. F.;
RT "Encephalogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";

RL J. Biol. Chem. 246:4630-4640(1971).
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
DR PROSITE; PS00569; MYELIN_MBP; PARTIAL.
KM Myelin; Structural protein; Autoimmune encephalomyelitis.
FT NON_TER 1 1
FT NON_TER 42 42
FT SEQUENCE 42 AA: 4537 MW: E283198F53F6DE73 CRC64;

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 42;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 DRGAPKRGSGRD 60
DB 4 DRGAPKRGSGRD 15

RESULT 9
MBP_CHICK ID MBP_CHICK STANDARD: PRT; 173 AA.

AC P15720;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
RX MEDLINE; 89358239.
RA Zopf D., Sonntag H., Betz H., Gundelfinger E. D.;
RT "Developmental accumulation and heterogeneity of myelin basic protein transcripts in the chick visual system.";
RL Glia 2:241-249(1989).
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X17103; CA834959.1; -.
DR PIR; S08535; S08535.
DR PIR; P01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELIN_MBP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KM Myelin; Structural protein; Acetylation; Methylation; Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 105 105 METHYLATION (BY SIMILARITY).
FT SEQUENCE 173 AA: 18677 MW: ABEF70D4C9CF019D CRC64;

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 173;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 OGTLKIRKLG 159
DB 148 OGTLKIRKLG 159

Db 146 OGTLKFKLGG 157

RESULT 10

ID MBP_RAJER STANDARD; PRT; 154 AA.

AC 091325;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE MYELIN BASIC PROTEIN (MBP).

GN MBP.

OS Raja erinacea (Little skate).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Neoselachii; Squalae; Hypnosqualae; Pristigastera;

OC Batoidae; Rajiformes; Rajidae; Rajae; Raja.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN, AND SPINAL CORD;

RX MEDLINE: 94016687.

RA SPIVACK W.D., Zhong N., Salerno S., Saavedra R.A., Gould R.M.;

RT Molecular cloning of the myelin basic proteins in the shark, Squalus

acanthias, and the ray, Raja erinacea."

RL J. Neurosci. Res. 35:577-584(1993).

CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE

OF MYELIN.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.

CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.

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CC -----

DR EMBL: U44053; AAA96756.1; -

DR PRAM; P01669; Myelin_MBP.1.

DR PRINTS; P00212; MYELINMBP.

DR PROSITE; PS00569; MYELIN_MBP.1.

KM Myelin; structural protein; Acetylation; Phosphorylation.

FT INIT_MET 0 1 ACETYLATION (BY SIMILARITY).

FT MOD_RES 1 1 K -> Q.

FT VARIANT 30 30 K -> R.

SQ SEQUENCE 154 AA; 16451 MW; 30A0ED482B4BA681 CRC64;

Query Match 4.7%; Score 8; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 PVVHFFKN 93

Db 73 PVVHFFKN 80

RESULT 11

ID MBP_SQUAC STANDARD; PRT; 154 AA.

AC 091439;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE MYELIN BASIC PROTEIN (MBP).

GN MBP.

OS Squalus acanthias (Spiny dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Neoselachii; Squalae; Squaloidae; Squalidae; Squalus.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN, AND SPINAL CORD;

RX MEDLINE: 94016687.

RA SPIVACK W.D., Zhong N., Salerno S., Saavedra R.A., Gould R.M.;

RT Molecular cloning of the myelin basic proteins in the shark, Squalus

acanthias, and the ray, Raja erinacea."

RL J. Neurosci. Res. 35:577-584(1993).

CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE

OF MYELIN.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.

CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.

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CC -----

DR EMBL: U44052; AAA96757.1; -

DR PRAM; P01669; Myelin_MBP.1.

DR PRINTS; P00212; MYELINMBP.

DR PROSITE; PS00569; MYELIN_MBP.1.

KM Myelin; structural protein; Acetylation; Phosphorylation.

FT INIT_MET 0 1 ACETYLATION (BY SIMILARITY).

FT MOD_RES 1 1 K -> Q.

SQ SEQUENCE 154 AA; 16479 MW; C129F8A824ABBC93 CRC64;

Query Match 4.7%; Score 8; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 PVVHFFKN 93

Db 73 PVVHFFKN 80

RESULT 12

ID PCP3_AMPCA STANDARD; PRT; 323 AA.

AC P80483;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE PERIDININ-CHLOROPHYLL A BINDING PROTEIN 3 (PCP).

OS Amphidinium carterae (Dinoflagellate).

OC Eukaryota; Alveolata; Dinophyceae; Gymnodiniales; Gymnodinaceae;

OC Amphidinium.

[1]

RP PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN-CS-21;

RX MEDLINE: 96413810.

RA Sharples F.P., Wrench P.M., Ou K., Hiller R.G.;

RT "Two distinct forms of the peridinin-chlorophyll a-protein from

Amphidinium carterae."

RT Blochm. Biophys. Acta 1276:117-123(1996).

CC -1- FUNCTION: WATER-SOLUBLE ANTENNA FOR CAPTURE OF SOLAR ENERGY IN THE

CC BLUE-GREEN RANGE. PERIDININ IS AN ASYMMETRIC CAROTENOID HAVING A

CC MAXIMUM ABSORPTION AT APPROXIMATELY 480 NM.

CC -1- DOMAIN: THE MATURE PROTEIN IS COMPOSED OF 2 ALMOST IDENTICAL

CC REPEAT UNITS.

DR HSSP; P80484; 1PPR.

KM Light-harvesting polypeptide; Chloroplast; Multigene family; Repeat.

FT SITE 70 70 CHLOROPHYLL A-BINDING.

FT SITE 244 244 CHLOROPHYLL A-BINDING.

FT REPEAT 1 1.

SQ SEQUENCE 323 AA; 34230 MW; 478FB2DE2E3E2343 CRC64;

Query Match 4.7%; Score 8; DB 1; Length 323;

Best Local Similarity 100.0%; Pred. No. 0.86;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SKYLATAS 20

Db 204 SKYLATAS 211

RESULT 13

MBP_HETFR MBP_HETFR STANDARD; PRT; 154 AA.

AC P20939;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE MYELIN BASIC PROTEIN (MBP).

OS Heterodontus francisci (Horn shark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Neoselachii; Galeomorphii; Heterodontoidae;

OC Heterodontiformes; Heterodontidae; Heterodontus.

CC [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN:

RX MEDLINE: 90040744.

RA Sanders J., Hood L., Abersold R.H., Arden B., Horvath S.,

RT "The myelin proteins of the shark brain are similar to the myelin

RT proteins of the mammalian peripheral nervous system."

RL J. Mol. Evol. 29:149-156(1989).

CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE

CC OF MYELIN.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.

CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.

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CC -----

DR EMBL: X17664; CA35661.1; -

DR PIR: B32999; B32999.

DR PRAM: PFO1669; Myelin_MBP; 1.

DR PRINTS: PRO0212; MYELINMBP.

DR PROSITE: PS00569; MYELIN_MBP; 1.

KW Myelin, structural protein; Acetylation; Phosphorylation.

FT INIT_MET 0

FT MOD_RES 1

SQ SEQUENCE 154 AA; 16502 MW; A9A57DA149429A83 CRC64;

Query Match 4.1%; Score 7; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 VVHEFFKN 93

Db 74 VVHEFFKN 80

RESULT 14

YGY3_YEAST YGY3_YEAST STANDARD; PRT; 368 AA.

AC P53295;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-1999 (Rel. 38, Last annotation update)

DE HYPOTHETICAL 41.0 KDA PROTEIN IN YIP1-CBP4 INTERGENIC REGION.

GN YGRI17M.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]

RP SEQUENCE FROM N.A.

RA Hebling U., Hofmann B., Deltus H.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE GTP1/ORG FAMILY.

CC -----

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CC -----

DR EMBL: Z72958; CA97199.1; -

DR PRAM: PFO1018; GTP1_ORG; 1.

DR PRINTS: PRO0326; GTP1_ORG; 1.

DR PROSITE: PS00905; GTP1_ORG; 1.

KW Hypothetical protein; GTP-binding.

FT NP_BIND 70 77 GTP (BY SIMILARITY).

FT NP_BIND 116 120 GTP (BY SIMILARITY).

FT NP_BIND 250 253 GTP (BY SIMILARITY).

SQ SEQUENCE 368 AA; 41006 MW; D144569C9C5D777C CRC64;

Query Match 4.1%; Score 7; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 SQKGRG 109

Db 125 SQKGRG 131

RESULT 15

LBP_RAT LBP_RAT STANDARD; PRT; 481 AA.

AC 063313;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP).

GN LBP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;

RX MEDLINE: 94292804.

RA Su G.L., Freeswick P.D., Geller D.A., Wang Q., Shapiro R.A., Wan Y.H.,

RT "Molecular cloning, characterization, and tissue distribution of rat

RT lipopolysaccharide binding protein. Evidence for extrahapatic

RT expression."

RL J. Immunol. 153:743-752(1994).

CC -1- FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL

CC LIPOPOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE OUTER

CC MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS

CC TO INTERACT WITH THE CD14 RECEPTOR.

CC -1- SIMILARITY: BELONGS TO THE BPI/CEP/LBP/PLTP FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: L32132; AAA21835.1; -

DR HSSP: P17213; LBPI.

DR PFAM: PF01273; LBP_BPI_CETP; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; 1.
KW Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 481 LIPOLYSACCHARIDE-BINDING PROTEIN.
FT CARBOHYD 300 300 POTENTIAL.
FT CARBOHYD 355 355 POTENTIAL.
SQ SEQUENCE 481 AA; 53600 MW; 23E67CB9CC97D2FC CRC64;

Query Match 4.1%; Score 7; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 GRGLSL 113
Db 98 GRGLSL 104

Search completed: September 26, 2000, 19:38:14
Job time: 111 sec

Result	Score	Query No.	Match Length	DB	ID	Description
1	171	100.0	304	4	Q15340	Q15340 homo sapien
2	59	34.5	137	4	Q15339	Q15339 homo sapien
3	46	26.9	154	11	Q9Z1U5	Q9Z1U5 rattus nor
4	46	26.9	159	11	Q9Z1U5	Q9Z1U5 rattus nor
5	46	26.9	135	11	Q9Z1U4	Q9Z1U4 rattus nor
6	34	19.9	139	11	Q61836	Q61836 mus muscul
7	34	19.9	135	11	Q01585	Q01585 mus muscul
8	34	19.9	250	11	Q03139	Q03139 mus muscul
9	17	9.9	34	11	Q61837	Q61837 mus muscul
10	8	4.7	176	13	P87346	P87346 xenopus la
11	8	4.7	281	10	Q38690	Q38690 amphidinlu
12	7	4.1	87	12	Q69559	Q69559 human herp
13	7	4.1	88	12	Q69559	Q69559 human herp
14	7	4.1	93	12	Q9W440	Q9W440 human herp
15	7	4.1	93	12	Q69048	Q69048 human herp
16	7	4.1	133	2	Q31793	Q31793 bacillus su
17	7	4.1	140	10	Q9KFE2	Q9KFE2 oryza sat
18	7	4.1	259	5	Q21174	Q21174 caenorhabd
19	7	4.1	259	12	Q298438	Q298438 paramelunc
			332	2	Q67104	Q67104 aquileo

20	7	4.1	364	13	057346	057346 oncoerythrin
21	7	4.1	545	10	080750	080750 arabidopsis
22	7	4.1	565	12	039290	039290 equine herp
23	7	4.1	813	2	087964	087964 thermotoga
24	7	4.1	1151	13	057580	057580 gallus galli
25	7	4.1	1344	12	069071	069071 human herpes
26	6	3.5	45	12	039703	039703 polyomavir
27	6	3.5	59	13	091419	091419 gallus galli
28	6	3.5	71	12	012311	012311 hepatitis g
29	6	3.5	72	2	066174	066174 agrobacteri
30	6	3.5	72	2	092484	092484 agrobacteri
31	6	3.5	89	4	043185	043185 homo sapien
32	6	3.5	96	2	051168	051168 borella bu
33	6	3.5	102	3	012047	012047 saccharomyc
34	6	3.5	103	12	055294	055294 hepatitis g
35	6	3.5	103	12	055295	055295 hepatitis g
36	6	3.5	103	12	055299	055299 hepatitis g
37	6	3.5	103	12	055303	055303 hepatitis g
38	6	3.5	103	12	055310	055310 hepatitis g
39	6	3.5	103	12	055311	055311 hepatitis g
40	6	3.5	103	12	055314	055314 hepatitis g
41	6	3.5	104	10	055316	055316 hepatitis g
42	6	3.5	104	10	042244	042244 arabidopsis
43	6	3.5	109	2	09X292	09X292 thermotoga
44	6	3.5	111	12	082080	082080 hame rhab
45	6	3.5	111	13	09YH66	09YH66 brachydanio

ALIGNMENTS

RESULT	1
Q15340	
ID	Q15340
AC	Q15340;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE	GGOL1-MBP.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-BRAIN;
RX	MEDLINE: 94068468.
RA	PICBYL T.M., CAMPAGNONI C.W., KAMPE K., KASHIMA T., HANDLEY V.W.,
RA	MACAONON J., CAMPAGNONI A.T.;
RT	"The human myelin basic protein gene is included within a 179-kilobase
RT	transcription unit: expression in the immune and central nervous
RT	systems."
DR	EMBL; L18866; AAA72011.1; -.
DR	PROSITE: PS00569; MYELIN.MBP; 1.
DR	PRINTS; PR00212; MYELINMBP.
Q0	SEQUENCE 304 AA: 3317 MW; 4E98B0AE CRC32;

Query Match	100.0%;	Score 171;	DB 4;	Length 304;
Best Local Similarity	100.0%;	Pred. No. 4.6e-175;		
Matches 171; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MASQKRP	SQRHGS	KYLAT	TASTMD	ARGCLF	PRNRD	IT	ILDS	IGFF	GGD	GAP	RGS	GKD	60
Dd	134	MASQKRP <td>SQRHGS <td>KYLAT <td>TASTMD <td>ARGCLF <td>PRNRD <td>IT <td>ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td></td></td></td></td></td></td></td>	SQRHGS <td>KYLAT <td>TASTMD <td>ARGCLF <td>PRNRD <td>IT <td>ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td></td></td></td></td></td></td>	KYLAT <td>TASTMD <td>ARGCLF <td>PRNRD <td>IT <td>ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td></td></td></td></td></td>	TASTMD <td>ARGCLF <td>PRNRD <td>IT <td>ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td></td></td></td></td>	ARGCLF <td>PRNRD <td>IT <td>ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td></td></td></td>	PRNRD <td>IT <td>ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td></td></td>	IT <td>ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td></td>	ILDS <td>IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td></td>	IGFF <td>GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td></td>	GGD <td>GAP <td>RGS <td>GKD</td> <td>193</td> </td></td>	GAP <td>RGS <td>GKD</td> <td>193</td> </td>	RGS <td>GKD</td> <td>193</td>	GKD	193
QY	61	SHNPART <td>AH</td> <td>TGSL</td> <td>PQK</td> <td>SHG</td> <td>RTQ</td> <td>EN</td> <td>PV</td> <td>HE</td> <td>F</td> <td>K</td> <td>N</td> <td>I</td> <td>120</td>	AH	TGSL	PQK	SHG	RTQ	EN	PV	HE	F	K	N	I	120
Dd	194	SHNPART <td>AH</td> <td>TGSL</td> <td>PQK</td> <td>SHG</td> <td>RTQ</td> <td>EN</td> <td>PV</td> <td>HE</td> <td>F</td> <td>K</td> <td>N</td> <td>I</td> <td>253</td>	AH	TGSL	PQK	SHG	RTQ	EN	PV	HE	F	K	N	I	253
QY	121	GQRG	F	FG	G	A	S	D	Y	K	A	H	G	F	171
Dd	254	GQRG	F	FG	G	A	S	D	Y	K	A	H	G	F	304

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RESULT 2
Q15339 ID 015339 PRELIMINARY; PRT; 197 AA.
AC 015339;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE GOLLI-MBP.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94068468.
RA PIRBYL T.M., CAMPAGNONI C.W., KAMPE K., KASHIMA T., HANDLEY V.W.,
RA MCMAHON J., CAMPAGNONI A.T.;
RT "The human myelin basic protein gene is included within a 179-kilobase
RT transcription unit: expression in the immune and central nervous
RT systems."
RL PROC. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993).
DR EMBL: L18865; AAA72010.1; -.
SQ SEQUENCE 197 AA; 21522 MW; D8A8A5BF CRC32;

Query Match 34.5%; Score 59; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.8e-55;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFGDGRGAPKRSCK 59
Db 134 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFGDGRGAPKRSCK 192

RESULT 3
Q92136 ID 092136 PRELIMINARY; PRT; 154 AA.
AC 092136;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE MYELIN BASIC PROTEIN.
GN MBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LEWIS RAT;
RA LOBELLE A.M., WIGZELL H.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A132896; CA10805.1; -.
DR PROSITE: PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 154 AA; 17207 MW; F3971E0B CRC32;

Query Match 26.9%; Score 46; DB 11; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.9e-41;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFG 46
Db 1 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFG 46

RESULT 4
Q92135 ID 092135 PRELIMINARY; PRT; 169 AA.
AC 092135;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DR PROSITE: PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 169 AA; 18470 MW; B0A7C0A0 CRC32;
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DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE MYELIN BASIC PROTEIN.
GN MBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LEWIS RAT;
RA LOBELLE A.M., WIGZELL H.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A132897; CA10806.1; -.
DR PROSITE: PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 169 AA; 18470 MW; B0A7C0A0 CRC32;

Query Match 26.9%; Score 46; DB 11; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.1e-41;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFG 46
Db 1 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFG 46

RESULT 5
Q92134 ID 092134 PRELIMINARY; PRT; 195 AA.
AC 092134;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE MYELIN BASIC PROTEIN.
GN MBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LEWIS RAT;
RA LOBELLE A.M., WIGZELL H.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A132898; CA10807.1; -.
DR PROSITE: PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 195 AA; 21484 MW; 79E52D9D CRC32;

Query Match 26.9%; Score 46; DB 11; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFG 46
Db 1 MASQKRPQSRHSGSKYLATASTMDHARGFLPRHRDTGILDSIGRFG 46

RESULT 6
Q61836 ID 061836 PRELIMINARY; PRT; 149 AA.
AC 061836;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE MYELIN BASIC PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-BRAIN;
RX MEDLINE: 87118269.
RA NEWMAN S., KITAMURA K., CAMPAGNONI A.T.;
RT "Identification of a cDNA coding for a fifth form of myelin basic
```

RT protein in mouse."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).
 DR EMBL; M15062; AAB59712.1; -;
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Alternative splicing; Myelin.
 FT NON TER
 SQ SEQUENCE 149 AA; 16226 MW; A6DC1599 CRC32;

Query Match 19.9%; Score 34; DB 11; Length 149;
 Best Local Similarity 100.0%; Pred. No. 1.3e-28;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 SKYLATASTMDHARGFLPRHRDTGILDSIGRFF 46
 |||
 DB 2 SKYLATASTMDHARGFLPRHRDTGILDSIGRFF 35

RESULT 7

ID 001585 PRELIMINARY; PRT; 195 AA.
 AC 001585;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RP SEQUENCE FROM N.A.
 RC STRAIN-C57 BL/6J; TISSUE-BONE MARROW;
 RX MEDLINE; 93057537.
 RA GRIMA B., ZELENKA D., PESSAC B.;
 RT "A novel transcript overlapping the myelin basic protein gene."
 RL J. Neurochem. 59:2318-2323(1992).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-BRAIN;
 RX MEDLINE; 93186801.
 RA CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPE K.,
 RA AMR-DMARKEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBAR B.,
 RA KITAMURA K.;
 RT "Structure and developmental regulation of Goli-1-mbp, a 105-kilobase
 RT gene that encompasses the myelin basic protein gene and is expressed
 RT in cells in the oligodendrocyte lineage in the brain."
 RL J. Biol. Chem. 268:4930-4938(1993).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.

DR EMBL; X67319; CA447733.1; -;
 DR EMBL; I07508; AAA37721.1; -;
 DR MGI; MGI:96925; Mbp.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 SQ SEQUENCE 195 AA; 21004 MW; 557D83EA CRC32;

Query Match 19.9%; Score 34; DB 11; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.6e-28;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 SKYLATASTMDHARGFLPRHRDTGILDSIGRFF 46
 |||
 DB 144 SKYLATASTMDHARGFLPRHRDTGILDSIGRFF 177

RESULT 8

ID 003139 PRELIMINARY; PRT; 250 AA.
 AC 003139;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-BRAIN;
 RX MEDLINE; 93186801.
 RA CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPE K.,
 RA AMR-DMARKEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBAR B.,
 RA KITAMURA K.;
 RT "Structure and developmental regulation of Goli-1-mbp, a 105-kilobase
 RT gene that encompasses the myelin basic protein gene and is expressed
 RT in cells in the oligodendrocyte lineage in the brain."
 RL J. Biol. Chem. 268:4930-4938(1993).
 DR EMBL; I07507; AAA37720.1; -;
 DR PRINTS; PR00212; MYELINMBP.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 SQ SEQUENCE 250 AA; 27167 MW; 3A08ADF7 CRC32;

Query Match 19.9%; Score 34; DB 11; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-28;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 SKYLATASTMDHARGFLPRHRDTGILDSIGRFF 46
 |||
 DB 144 SKYLATASTMDHARGFLPRHRDTGILDSIGRFF 177

RESULT 9

ID 061837 PRELIMINARY; PRT; 34 AA.
 AC 061837;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MYELIN BASIC PROTEIN (FRAGMENT).
 GN SHI-MD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RP SEQUENCE FROM N.A.
 RX MEDLINE; 88186094.
 RA OKANO H., TAMURA T., MURA M., AOYAMA A., IKENAKA K., OSHIMURA M.,
 RA MIKOSHIBA K.;
 RT "Gene organization and transcription of duplicated MBP genes of myelin
 RT deficient (shi/mlld) mutant mouse."
 RL EMBO J. 7:77-83(1988).
 DR EMBL; M36275; AAA39504.1; -;
 DR PROSITE; PS00569; MYELIN_MBP; 1.

KW Myelin.
 FT NON TER
 FT NON TER
 SQ SEQUENCE 34 AA; 3958 MW; 31F53967 CRC32;

Query Match 9.9%; Score 17; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6e-11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 HGRIDENPVVHFFKNI 94
 |||
 DB 18 HGRIDENPVVHFFKNI 34

RESULT 10
 ID P87346 PRELIMINARY; PRT; 176 AA.
 DT P87346

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AC  P87346;
DT  01-MAY-1997 (TReMBLrel. 03, Created)
DT  01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DE  01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE  MYELIN BASIC PROTEIN.
OC  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC  Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae;
OC  Xenopus.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-J; TISSUE-BRAIN;
RA  NAGATA S., OGINO K.;
RT  "CDNA for Xenopus laevis myelin basic protein.";
RL  Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; A8000736; BAA19174.1; -.
DR  PRINTS; PR00212; MYELINBP.
KM  Myelin.
SQ  SEQUENCE 176 AA; 19720 MW; AB3F06B CRC32;

Query Match 4.7%; Score 8; DB 13; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  97 PRTPPSQ 104
    |||||
DB  101 PRTPPSQ 108

RESULT 11
ID  Q38690 PRELIMINARY; PRT; 281 AA.
AC  Q38690;
DT  01-NOV-1996 (TReMBLrel. 01, Created)
DT  01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE  01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE  HIGH SALI PERIDININ-CHLOROPHYLL A-PROTEIN (FRAGMENT).
OC  Amphidinium carterae (Dinoflagellate).
OC  Eukaryota; Alveolata; Dinophyceae; Gymnodiniales; Gymnodinaceae;
OC  Amphidinium.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CS 21;
RA  SHARPLES F.P., WRENCH P.M., OU K., HILLER R.G.;
RL  Biochim. Biophys. Acta 0:0-0(1996).
DR  EMBL; 271600; CAA96255.1; -.
DR  MENDEL; 16839; Ampca; 2754; 16839.
FT  NON_TER 1 281
FT  NON_TER 1 281
SQ  SEQUENCE 281 AA; 29946 MW; 98FD660F CRC32;

Query Match 4.7%; Score 8; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  13 SKYLATAS 20
    |||||
DB  184 SKYLATAS 191

RESULT 12
ID  Q69559 PRELIMINARY; PRT; 87 AA.
AC  Q69559;
DT  01-NOV-1996 (TReMBLrel. 01, Created)
DT  01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE  01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE  U24, GLYCOPROTEIN.
GN  U24.
OS  Human herpesvirus 6.
OS  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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OC  Betaherpesvirinae; Roseolovirus.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 95266321.
RA  GOMPELS U.A., NICHOLAS J., LAWRENCE G., JONES M., THOMSON B.J.,
RA  MARTIN M.E., EFSTATHIOU S., CRAXTON M., MACMULLEN H.A.;
RT  "The DNA sequence of human herpesvirus-6: structure, coding content,
RT  and genome evolution."
RL  J. Virol. 209:29-51(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 90080132.
RA  LAWRENCE G.L., CHEE M., CRAXTON M.A., GOMPELS U.A., HONESS R.W.,
RA  BARRELL B.G.;
RT  "Human herpesvirus 6 is closely related to human cytomegalovirus.";
RL  J. Virol. 64:287-299(1990).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 91237802.
RA  CHANG C.K., BALACHANDRAN N.;
RT  "Identification, characterization, and sequence analysis of a CDNA
RT  encoding a phosphoprotein of human herpesvirus 6."
RL  J. Virol. 65:2884-2894(1991).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 91333007.
RA  TEO I.A., GRIFFIN B.E., JONES M.D.;
RT  Characterization of the DNA polymerase gene of human herpesvirus 6."
RL  J. Virol. 65:4670-4680(1991).
RN  [5]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 9126542.
RA  THOMSON B.J., EFSTATHIOU S., HONESS R.W.;
RT  "Acquisition of the human adeno-associated virus type-2 rep gene by
RT  human herpesvirus type-6."
RL  Nature 351:78-80(1991).
RN  [6]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 91374590.
RA  MARTIN M.E.D., NICHOLAS J., THOMSON B.J., NEWMAN C., HONESS R.W.;
RT  "Identification of a transactivating function mapping to the putative
RT  immediate-early locus of human herpesvirus 6."
RL  J. Virol. 65:5381-5390(1991).
RN  [7]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 92333249.
RA  EFSTATHIOU S., LAWRENCE G.L., BROWN C.M., BARRELL B.G.;
RT  "Identification of homologues to the human cytomegalovirus US22 gene
RT  family in human herpesvirus 6."
RL  J. Gen. Virol. 73:1661-1671(1992).
RN  [8]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 92146942.
RA  GENG Y., CHANDRAN B., JOSEPHS S.F., WOOD C.;
RT  "Identification and characterization of a human herpesvirus 6 gene 1
RT  promoter."
RL  J. Virol. 66:1564-1570(1992).
RN  [9]
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RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 93091236.
RA  GOMPELS U.A., CARSS A.L., SUN N., ARRAND J.R.;
RT  "Infectivity determinants encoded in a conserved gene block of human
RT  herpesvirus-6."

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RL DNA Seq 3:25-39(1992).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 92260671.
 RA NEIPEL F., ELLINGER K., FLECKENSTEIN B.;
 RT "Gene for the major antigenic structural protein (p100) of human
 RL herpesvirus 6.";
 RN J. Virol. 66:3918-3924(1992).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 923333248.
 RA THOMSON B.J., HONESS R.W.;
 RT "The right end of the unique region of the genome of human herpesvirus
 RL 6 U1102 contains a candidate immediate early gene enhancer and a
 J. Gen. Virol. 73:1649-1660(1992).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93187613.
 RA ELLINGER K., NEIPEL F., FOA-TOMASI L., CAMPADDELLI-FIOME G.,
 RT "The glycoprotein B homologue of human herpesvirus 6.";
 RL J. Gen. Virol. 74:495-500(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93224882.
 RA COMPELS U.A., CARRIGAN D.R., CARSS A.L., ARNO J.;
 RT "Two groups of human herpesvirus 6 identified by sequence analyses of
 RL laboratory strains and variants from Hodgkin's lymphoma and bone
 J. Gen. Virol. 74:613-622(1993).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93389439.
 RA LIU D.X., COMPELS U.A., NICHOLAS J., LELLIOTT C.;
 RT "Identification and expression of the human herpesvirus 6 glycoprotein
 RL H and interaction with an accessory 40K glycoprotein.";
 J. Gen. Virol. 74:1847-1857(1993).
 RN [15]
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 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 94025558.
 RA LIU D.X., COMPELS U.A., FOA-TOMASI L., CAMPADDELLI-FIOME G.;
 RT "Human herpesvirus-6 glycoprotein H and L homologs are components of
 RL the gp100 complex and the gH external domain is the target for
 neutralizing monoclonal antibodies.";
 J. Virol. 197:12-22(1993).
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 RX MEDLINE; 93331710.
 RA PELLETIER P.E., SANCHEZ-MARTINEZ D., DOMINGUEZ G., BLACK J.B., ANTON E.,
 RT GELLMAYER C., DARBACH T.R.;
 RL "A strongly immunoreactive viron protein of human herpesvirus 6
 variant B strain 229: Identification and characterization of the gene
 and mapping of a variant-specific monoclonal antibody reactive
 RL epitope.";
 J. Virol. 195:521-531(1993).
 RN [17]
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 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93323202.
 RA PEIPEPER B., BERNEMAN Z.N., NEIPEL F., CHANG C.K., TIRATAPONG S.,
 RT CHANDRAN B.;
 RL "Identification and mapping of the gene encoding the glycoprotein
 complex gp82-gp105 of human herpesvirus 6 and mapping of the
 neutralizing epitope recognized by monoclonal antibodies.";
 J. Virol. 67:4611-4620(1993).
 RL

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RN [18]
RP SEQUENCE FROM N.A.
RC STRAIN-U1102, VARIANT A;
RX MEDLINE; 95146989.
RA GOMPELS V.A., MACAULAY H.A.;
RT "Characterization of human telomeric repeat sequences from human
RL J. Gen. Virol. 76:451-458(1995).
RN [19]
RP SEQUENCE FROM N.A.
RC STRAIN-U1102, VARIANT A;
RX MEDLINE; 94047392.
RA DEHJUSST S., DOLLARD S.C., PELLET P.E., DAMBAUGH T.R.;
RT "Identification of a lytic-phase origin of DNA replication in human
RL J. Virol. 67:7680-7683(1993).
RN [20]
RP SEQUENCE FROM N.A.
RC STRAIN-U1102, VARIANT A;
RX NICHOLAS J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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RC STRAIN-U1102, VARIANT A;
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RA NICHOLAS J., MARTIN M.;
RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
RL genome of human herpesvirus 6 encoding human cytomegalovirus
RT immediate-early gene homologs and transactivating functions.";
RL J. Virol. 68:597-610(1994).
RN [22]
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RC STRAIN-U1102, VARIANT A;
RX MEDLINE; 94202284.
RA SCHIENE U., NEIPEL F., SCHREINER D., FLECKENSTEIN B.;
RT "Structure and transcription of an immediate-early region in the human
RL herpesvirus 6 genome.";
RL J. Virol. 68:2978-2985(1994).
RN [23]
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RX MEDLINE; 94181269.
RA THOMPSON J., CHOUDHURY S., KASHANCHI F., DONIGER J., BERNEMAN Z.,
RA FRANKEL N., ROSENTHAL L.J.;
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RX SUWAGAWA T., SASHIHARA J., ZOU P., KOSUGE H., YAMANISHI K.;
RT "A comparison of the complete DNA sequences between human herpesvirus-
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RT 6 variant A and B."
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 RX MEDLINE: 98044033.
 RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
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 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNETT S.C., BRON S.,
 RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPANO V., CARTER N.M.,
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 RA DENISOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
 RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOUGER D.,
 RA FRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZZI A., GALLERON N.,

RA CHIM S.Y., GLASER P., GOFFENAU A., GOLIGHTLY E.J., GRANDI G.,
 RA GUSEPPI G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A.,
 RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
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 RA LEE S.M., LEVINE A., LIT H., NASUDA S., MAUEL C., MEDIGUE C.,
 RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 RA NOONE D., O'REILLY M., OGAWA K., OGIMARA A., OUDEGA B., PARK S.H.,
 RA PARO V., POHL T.M., PORTELELLA D., POROMOLIK S., PRESCOTT A.M.,
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 RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKENARI K.,
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 RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
 RA VIARI A., WAMUTT R., WEDLER E., WEDLER H., WEITZEGGER T.,
 RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
 RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
 RN [2]
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 RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
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AUTHORS Bloembergen, H., Beecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE EST (Bloembergen, et al.)
JOURNAL Unpublished (1999)
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Contact: Bloembergen H
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Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZ564P227) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M.,
Suzuki, Y., Sasaki, M. and Sugano, S.
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REFERENCE
AUTHORS Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
Suzuki,Y., Sasaki,M. and Sugano,S.
TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
JOURNAL Unpublished (1999)
COMMENT On Jul 9, 1999 this sequence version replaced gi:5434934.
Contact: Katsuyuki Hashimoto
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-Ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.

FEATURES
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XhoI sites just outside the DraIII sites can be used to
isolate the cDNA insert. Size selection was performed by
exclude fragments <1.5 kb. Library was constructed by
Sugano et al. (University of Tokyo, Institute of Medical
Science). Custom primer for sequencing: 5' end primer
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
Suzuki,Y., Sasaki,M. and Sugano,S.
TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
JOURNAL Unpublished (1999)
COMMENT On Oct 8, 1998 this sequence version replaced gi:3727975.
Contact: Katsuyuki Hashimoto
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-Ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.

FEATURES
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/db_xref="taxon:10090"
/clone_lib="MNCB-3446"
/clone_1lb="Sugano mouse brain mncb"

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seq_name: gjb_est29:AU051764

34 rgAspThrGlyIleuAspSerIleGlyArgPheheGlyGlyAspArg 50
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142 GAGACACGGGCATCTTGACTCCATCGGGCCTCTTTAGGGGTGACAG 19

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seq.documentation_block:      779 bp      mRNA      EST      08-OCT-1998
LOCUS      AU035931
DEFINITION      AU035931 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-1058
                mRNA sequence.
ACCESSION      AU035931
VERSION        AU035931.1
KEYWORDS       EST.
SOURCE         house mouse.
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 779)
AUTHORS        Sasaki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibu,A., Yoshida,K.,
                Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
TITLE          Construction of mouse full length-enriched cDNA libraries
JOURNAL        Unpublished (1998)
COMMENT        Contact: Katsuyuki Hashimoto
                Division of Genetic Resources
                National Institute of Infectious Diseases
                23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
                Email: khashi@nih.go.jp.
                Location/Qualifiers
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            /strain="C57BL"
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            /sex="female"
            /dev_stage="adult"
            /lab_host="TOP10"
            /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                was primed with an oligo(dT) primer
                [ATGAGCCCTTTTCTTTTCTTTTCTTTT] double-stranded cDNA was
                ligated to a DraIII adaptor [TGTGGCTCTACTGG] , digested
                and cloned into distinct DraIII sites of the pME18S-FL3.
                XhoI sites just outside the DraIII sites can be used to
                isolate the cDNA insert. Size selection was performed by
                exclude fragments <1.5 Kb. library was constructed by

```

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237 TACCATTATGGCTCCCTGGCCCGAAGTCGACGACGGCGGACCCAG 286
|||||
83 sPGLIAsProValYalHisphelYelYsaInIleValThrProArGTMr 99
|||||
287 ATGAAACCCAGTATGCTCATTTCTTCAAGAACATGTGACACTCGAAC 336
|||||
100 ProProPserSerGlnGlyLysGlyArgGlyLeuSerLeuSerArpPhe 116
|||||
337 CCACCTCCATCCCAAGSAGSAGSAGSAGGCGCTGCTCCCTCAGCAGATTAG 386
|||||
116 rTPsPlylaaGluGlyGlnArGProGlyPheGlyTYrGlyGlyArgAla 133
|||||
387 CTGGGGGGCCGAGGGCGCAGAACCCAGATTTGGCTACGAGGCAGAGCTT 436
|||||
133 eAsPtyLylySerAlaHisLysGlyPheLysGlyVal..AspAlaGln 148
|||||
437 CGAATAAAATCGGCTCACAAAGGATTCAAAGGGGCGCTCGGCGCCAG 486
|||||
149 GLyThrLeuSerLysIlePheLysLeuGlyGlyArgAspSerArGserG 165
|||||
487 GCGACGCGCTTC.AAAATCTTTAACTGTGGAGGAAGAAGACAGCCGCTGTG 535
|||||
165 ySerPro 167
|||||
536 ATCTCCA 542
|||||

seq_name: qb_est29:AU051348

seq_documentation_block:
LOCUS AU051348 804 bp mRNA EST 18-MAR-1999
DEFINITION AU051348 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-19006
5', mRNA sequence.
ACCESSION AU051348
VERSION AU051348.1 GI:4434357
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
 1 (bases 1 to 804)
 Sasaki,M., Suzuki,Y., Watanabe,M., Imai,T., Shibui,A., Yoshida,K.,
 Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
 TITLE Construction of mouse full length-enriched cDNA libraries by
 oligo-capping
 JOURNAL Unpublished (1999)
 COMMENT On Jun 5, 1998 this sequence version replaced g1:3187684.
 CONTACT Katsuyuki Hashimoto
 Division of Genetic Resources
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: http://www.nih.go.jp/yoken/genbank/
 Seq primer: 5' end primer: CTTGCTCTTAAAGCTCGG.
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 /dev_stage="adult"
 /lab_host="TOP10"
 /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCTTTTCTTTTCTTTT] double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCTTACTGG] , digested
 and cloned into distinct DraIII sites of the pME18S-FL3.
 XhoI sites just outside the DraIII sites can be used to
 isolate the cDNA insert. Size selection was performed to
 exclude fragments <1.5 kb. Library was constructed by
 Sugano et al. (University of Tokyo, Institute of Medical
 Science). Custom primer for sequencing: 5' end primer
 [CTTGTCTTAAAGCTCGG]"

BASE COUNT 190 a 204 c 176 g 176 t 58 others
 ORIGIN

alignment_scores:
 Quality: 775.00 Length: 174
 Ratio: 4.784 Gaps: 5
 Percent Similarity: 93.103 Percent Identity: 89.080

alignment_block:
 US-09-218-277-12 x AU051348 ..

Align seg 1/1 to: AU051348 from: 1 to: 804

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1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
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47 ATGCGATCACAAGAGACCTCTACAGCGA.....TCCAAGTACTTGGC 90
|||||
17 aAthAlaSerTherMetAspHisAlaArgHisGlyPheLeuProAlaArgHisA 34
|||||
91 CACAGCAAGTACCATGACATGCCAGCATGGCTTCTCCCAAGGCCACA 140
|||||
34 tGAAPrtHrGlyLeuLeuAspSerIleGlyArgPhePheGlyLysAspArg 50
|||||
141 GAGACAGCGGCATCCTTACATCGGGCGCTTCTTAAAGGGTACAGG 190
|||||
51 GAlaAPrPolysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
|||||
191 GGTGGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC.....ACGAGAAC 234
|||||
67 tAlAHistyrGlySerLeuProGlnLysSer...HisGlyArgThrGlna 83
|||||
235 TACCATTATGGCTCCCTGCCCCAGAAAGTCCAGACGGCGGAGCCCAAG 284
|||||
83 spGUAsnProValValHisPhePheLysAsnIleValThrProArgThr 99
|||||
285 ATGAAGCCAGTAGTCCATTCTTCAAGAACATTGTGACACCTCGAACCA 334

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100 ProProSerSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPhe 116
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 335 CCACCTCCATCCCAAGGAGGAGGGAGCGCTGCTCCCTCAGCAGATTAG 384
 |||||
 116 rTPrGLyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAla 133
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 385 CTGGGGGGCCNAGGGGCGAAGCCAGGATTTGGCTACGGAGCGAGACT 434
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 133 eAspTyrLysSerAlaHisLysGlyPheLysGlyAla...AspAlaGln 148
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 435 CCGACTTAATATGGCTCACAAGAGGATTCAAGGGGGCTTACAGCCGAC 484
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seq_name: gb_est29:AU066815

seq_documentation_block:
 LOCUS AU066815 771 bp mRNA EST 02-JUN-1999
 DEFINITION AU066815 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-2602
 5', mRNA sequence.
 ACCESSION AU066815
 VERSION AU066815.1 GI:4967552
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 771)
 Sasaki,Y., Sasaki,M. and Sugano,S.
 TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
 library made by oligo-capping method
 JOURNAL Unpublished (1999)
 COMMENT On Apr 7, 1998 this sequence version replaced g1:3036368.
 CONTACT Katsuyuki Hashimoto
 Division of Genetic Resources
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: http://www.nih.go.jp/yoken/genbank/.

FEATURES
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 /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCTTTTCTTTTCTTTT] double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCTTACTGG] , digested
 and cloned into distinct DraIII sites of the pME18S-FL3.
 XhoI sites just outside the DraIII sites can be used to
 isolate the cDNA insert. Size selection was performed to
 exclude fragments <1.5 kb. Library was constructed by
 Sugano et al. (University of Tokyo, Institute of Medical
 Science). Custom primer for sequencing: 5' end primer
 [CTTGTCTTAAAGCTCGG]"

BASE COUNT 187 a 219 c 199 g 152 t 14 others
 ORIGIN

alignment_scores:

ligated to a DraIII adaptor (TGTGGCCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-R13. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTCTCTTAAAGCTGGG]"

BASE COUNT 184 a 225 c 201 g 151 t 9 others
ORIGIN

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Quality: 750.50 Length: 173
Ratio: 4.811 Gaps: 5
Percent Similarity: 90.173 Percent Identity: 86.705

alignment_block:
US-09-218-277-12 x AU066924 ..

Align seg 1/1 to: AU066924 from: 1 to: 770

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|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
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92 CACAGCAGTACCATGACATGACATGACATGCTCTCCCAAGGCACA 141
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34 rGAspThrGlyLeuAspSerLysGlyArgPhePheGlyLysAspArg 50
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142 GAGAACGGGCGATCCTTGACTCCATCGGGCGCTTTAGCGGTGACAG 191
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51 GYAlaProLysArgLysSerGlyLysAspSerHisProAlaArgTh 67
|||||
192 GGTGGGCCCAAGCGGGCTCTGCAAGACTCAC.....ACGAGAAC 235
|||||
67 rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGln 83
|||||
236 TACCCTATATGGCTCCCTGCCCAAGATCGACGACGCGGACCCAG 285
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83 sPGLAsnProValAlaHisPhePhePheLysAsnLleValThrProArg 99
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286 ATGAAACCCAGTATGCTCATTTCTTCAAGACATGTGTGACACCTCG 335
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100 ProProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPhe 116
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336 CCACCTCCATCCCAAGGAG..... 356
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116 rTrpGlyAlaGlnGlyGlnArgProGlyPheGlyTyrGlyArgAla 133
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357 ...GGGGCCGAGGGGAGAGCCAGGATTGGCTACGAGAGAGCTT 402
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133 eTrAspTyrTrpSerAlaHisLysGlyPheLysGlyAla...AspAla 148
|||||
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|||||
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453 GGCACGCTTCCAAAATCTTTAAAGCTGGAGAGAGAGACGCCCTCTG 502
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LOCUS AA352612 511 bp mRNA EST 21-Apr-1997
DEFINITION EST60632 Activated T-cells xx Homo sapiens cDNA 5' end similar to
myelin basic protein, mRNA sequence.
ACCESSION AA352612

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VERSION AA352612.1 GI:2004932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 511)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bull,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geophagen,N.S.,
Kelley,U.M., Kelley,U.C., Liu,L.-I., Marmaro,S.M., Merrick,U.M.,
Moreno-Palmarques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrite,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,R.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
12140200
COMMENT Other ESTs: THC171045
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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location/Qualifiers
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/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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BASE COUNT 124 a 141 c 145 g 89 t 12 others
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Quality: 749.00 Length: 160
Ratio: 4.993 Gaps: 2
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alignment_block:
US-09-218-277-12 x AA352612 ..

Align seg 1/1 to: AA352612 from: 1 to: 511

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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
86 CACAGCAGTACCATGACATGACATGACATGCTCTCCCAAGGCACA 135
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34 rGAspThrGlyLeuAspSerLysGlyArgPhePheGlyLysAspArg 50
|||||

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|||||
136 GAGACAGGGCATCNTGACTCCATCGGGCGCTTCTTGCGGGTGAACG 185
51 GLYALAProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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186 GGTGCGCGCTAATCGGGGCTCTGGCAAGACTNACACCACCGGCAAGAAC 235
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
236 TGCTCACTATGGCTCCTGCCCCAGAAAGTCACAGGGCGGAGCCCAAGATG 285
84 LuAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
|||||
286 AAACCCCGTAGTCACACTTCTCAAGAACATNTMGACCGCTNGACACACA 335
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
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336 CCCCCTGTCAGGGAAGGGAGAGGACTGCTCCCTGAGCAGATTAGCTG 385
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSerA 134
|||||
386 GGGGGCCGAANAGTAGNACCAGGATTTGGCTACGGAGGAGGAGCGTCCG 435
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyTh 150
|||||
436 ACTATAATCGGNTCACAGGNTTCAAGGAGTTCATGTCATGNCACAGGNA 485
150 rLeuSerLysIlePheLysLeuGly 158
|||||
486 GTTTTCAAAAATTTTAAAGTTGGG 511
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2000, 17:47:28 ; Search time 40.8 Seconds
(without alignments)
99.273 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 922
Sequence: 1 MASQRRPSQRHSGKYLATAS.....SKTFKLGDRSGSPMARR 171

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	922	100.0	171	1 R97627	Human myelin basic
2	922	100.0	171	1 R99580	Human myelin basic
3	917	99.5	170	1 R8592	Human myelin basic
4	917	99.5	170	1 R95406	Myelin oligodendro
5	909	98.6	170	1 R35440	Human basic myelin
6	899	97.5	197	1 W00399	Human myelin basic
7	899	97.5	203	1 W06107	Foetal myelin basi
8	899	97.5	203	1 W06108	Foetal myelin basi
9	899	97.5	373	1 W06103	MP4 chimera (MBP21
10	899	97.5	385	1 W06102	MP3 chimera (MBP21
11	899	97.5	492	1 W06105	MMOGP4 chimera (MB
12	894	97.0	375	1 W06104	PM4 chimera (delta
13	891	96.6	170	1 R30736	Human MBP. Pure ma
14	855	92.7	168	1 R04717	Empirically determ
15	832	90.2	168	1 R48594	Rabbit myelin basi
16	822.5	89.3	169	1 R48593	Cattle myelin basi
17	814.5	88.3	170	1 R02226	Myelin basic prote
18	814.5	88.3	170	1 R30735	Bovine MBP. Pure m
19	814.5	88.3	170	1 W57236	Myelin basic prote
20	798.5	86.6	170	1 R86422	Myelin basic prote
21	797.5	86.5	170	1 R45947	Myelin basic prote
22	779.5	84.5	167	1 R48595	Myelin basic prote
23	603.5	65.5	127	1 R48596	Rat myelin basic p
24	534	57.9	170	1 R48597	Chicken myelin bas
25	260	28.2	46	1 W72360	Human myelin basic
26	162	17.6	32	1 R85138	Human MBP residues
27	162	17.6	32	1 R95369	Residues 139-170 o
28	140	15.2	25	1 R95367	Residues 111-135 o
29	139	15.1	25	1 R95342	MBP-2.5 (80-104) .
30	139	15.1	25	1 W43948	Human myelin basic
31	136	14.8	25	1 R95347	MBP-5 (101-125) . M
32	136	14.8	25	1 W43953	Human myelin basic
33	135	14.8	24	1 R49336	Myelin basic prote

34	135	14.6	24	1 R74158	Antigenic peptide
35	135	14.6	24	1 W54719	Peptide from Myelin
36	135	14.6	27	1 R95372	Residues 142-168 o
37	134	14.5	24	1 R95338	MBP-2.1 (82-105) .
38	134	14.5	24	1 W37554	Human myelin basic
39	134	14.5	207	1 W10493	Soluble fused MHC
40	129	14.0	23	1 R95339	MBP-2.2 (82-104) .
41	129	14.0	23	1 W37555	Human myelin basic
42	128	13.9	23	1 R85137	Human MBP residues
43	128	13.9	23	1 R95343	MBP-2.6 (80-102) .
44	128	13.9	23	1 R95337	MBP-2 (83-105) . My
45	128	13.9	23	1 W44072	Human myelin basic

ALIGNMENTS

RESULT 1	
R97627	188963 seqs, 23686106 residues
ID	R97627 standard; Protein; 171 AA.
AC	R97627;
DT	09-NOV-1996 (first entry)
DE	Human myelin basic protein.
KW	Myelin basic protein; MBP; multiple sclerosis; MS; treatment;
KW	prevention; analogue.
OS	Homo sapiens.
FT	Key
FT	Location/Qualifiers
FT	peptide 86..99
FT	/label= Claimed peptide region.
FN	W09616085-A1.
PD	30-MAY-1996.
PF	16-NOV-1995; U14402.
PR	18-NOV-1994; US-342078.
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.
PI	(STRD) UNIV STANFORD MEDICAL CENT.
PI	Conlon PJ, Gaur A, Ling N, Steinman L;
DR	WPL; 96-288534/27.
DR	N-PSDB; T30269.
PT	Peptide analogue of human myelin basic protein - has lysine 91
PT	replaced by another amino acid, useful to treat multiple sclerosis
PS	Claim 1: Figure 1, 30pp; English.
CC	A peptide analogue comprising amino acids 87-99 of human myelin
CC	basic protein (MBP), where Lys91 is substituted for another amino
CC	acid can be used to treat and prevent multiple sclerosis. The
CC	peptide analogue is administered at a dosage range of 5-50 mg/Kg.
SQ	Sequence 171 AA;
Query Match	100.0%; Score 922; DB 1; Length 171;
Best Local Similarity	100.0%; Pred. No. 3.1e-90;
Matches 171; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DB	1 MASQRRPSQRHSGKYLATASMDARHGFELPRHNDTGILDSIGRFGGDRCAPRRGSGKD 60
OY	61 SHHPRATHYSLPQKSGRTQDENPVVHFKNVTPTPTPPSGKGGLSLRFSWGAE 120
DB	61 SHHPRATHYSLPQKSGRTQDENPVVHFKNVTPTPTPPSGKGGLSLRFSWGAE 120
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DB	121 GORPFGYGRASDYKSAHKGFGVDAQGLSKTFKLGRDSRSGSPMARR 171
RESULT 2	
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ID	R99580 standard; Protein; 171 AA.
AC	R99580;
DT	07-NOV-1996 (first entry)
DE	Human myelin basic protein (MBP).
KW	Myelin basic protein; MBP; multiple sclerosis; MS; competition;
KW	inhibition; major histocompatibility complex; MHC; thymocyte; T cell;

KW experimental allergic encephalomyelitis; EAE; analogue.
OS Homo sapiens.
PN WO9616086-A1.
PD 30-MAY-1996.
PF 16-NOV-1995; U14403.
PR 18-NOV-1994; US-342408.
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
PI Conlon PJ, Gaur A, Ling N, Steinman L;
DR MPI; 96-268535/27.
DR N-PSDB; T32561.
PT Peptide analogues of human myelin basic protein - useful for
PS treatment of multiple sclerosis
PS Disclosure: Figure 1; 61pp; English.
CC Peptide analogues comprising at least seven amino acids from
CC residues 86-99 of human myelin basic protein (MBP), can be used to
CC treat multiple sclerosis by competing for the binding of native MBP
CC peptide to MHC and by not causing proliferation of an MBP reactive T-
CC cell line. The peptide analogues also inhibit the induction of
CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.
CC The peptide analogues have a reduced susceptibility to proteolysis
CC in vivo.
SO Sequence 171 AA;

Query Match 100.0%; Score 922; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 3.1e-90;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASOKRPSORHGSKYLTASTMDHARHGFLPRHRDGTILDSIGRFGDGDGAPRSGSKD 60
DB 1 MASOKRPSORHGSKYLTASTMDHARHGFLPRHRDGTILDSIGRFGDGDGAPRSGSKD 60
QY 61 SHHPARTAHYGSLEPQKSHGRTODENPVVHEFKNIIVTPRTPPPSGKRGSLSRFSWGAE 120
DB 61 SHHPARTAHYGSLEPQKSHGRTODENPVVHEFKNIIVTPRTPPPSGKRGSLSRFSWGAE 120
QY 121 GQRFGFYGRASDYKSAHKGFGVDAGTILSKIFKIGSGDSRSGSPMAR 171
DB 121 GQRFGFYGRASDYKSAHKGFGVDAGTILSKIFKIGSGDSRSGSPMAR 171

RESULT 3
R48592
ID R48592 standard; protein; 170 AA.
AC R48592;
DE 31-JUL-1994 (first entry)
KW Human myelin basic protein.
KW Protolipid protein; myelin basic protein; retrovirus;
KW neurological disease; by-stander antigen; TGF-beta;
KW transforming growth factor-beta; T-cell; T-lymphocyte;
KW myelopathy; paraparesis; human immunodeficiency virus type 1.
OS Homo sapiens.
PN WO9404121-A.
PD 03-MAR-1994.
PF 17-AUG-1993; U07786.
PR 17-AUG-1992; US-931217.
PA (AUTO-) AUTOIMMUNE INC.
PI Hafner DA, Weiner HL;
DR MPI; 94-082786/10.
PT Treating retroviral associated neurological disease - by admin.
PS of by-stander antigen, causing release of transforming growth
PS factor beta from suppressor T cells
PS Disclosure: Page 49; 64pp; English.
CC Myelin basic proteins (sequences R48592-96) and cattle proteolipid
CC protein (R48592) elicit the release of TGF-beta from suppressor T-
CC cells and target the T-cells to neural tissue under cytotoxic
CC attack, thereby reducing neurological disease, e.g. HIV-1
CC associated myelopathy, tropical spastic paraparesis and HIV
CC infection.
SO Sequence 170 AA;

Query Match 99.5%; Score 917; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 1e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDGTILDSIGRFGDGDGAPRSGSKD 61
DB 1 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDGTILDSIGRFGDGDGAPRSGSKD 60
QY 62 HHPTARTAHYGSLEPQKSHGRTODENPVVHEFKNIIVTPRTPPPSGKRGSLSRFSWGAE 121
DB 62 HHPTARTAHYGSLEPQKSHGRTODENPVVHEFKNIIVTPRTPPPSGKRGSLSRFSWGAE 120
QY 122 GQRFGFYGRASDYKSAHKGFGVDAGTILSKIFKIGSGDSRSGSPMAR 171
DB 121 GQRFGFYGRASDYKSAHKGFGVDAGTILSKIFKIGSGDSRSGSPMAR 170

RESULT 4
R95406
ID R95406 standard; protein; 170 AA.
AC R95406;
DE 16-DEC-1996 (first entry)
KW Myelin oligodendrocyte protein.
KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
KW CD4+, T-cell; autoimmune disease; demyelination; central nervous system;
KW CNS; animal model; human; multiple sclerosis; MS; mammal; Denglin MS; MOG;
KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
OS Homo sapiens.
PN WO9612737-A2.
PD 02-MAY-1996.
PR 25-OCT-1995; U13682.
PR 25-OCT-1994; US-328224.
PR 15-MAR-1995; US-404228.
PR 25-OCT-1995; ZA-009033.
PA (IMMU-) IMMUNOLOGIC PHARM CORP.
PI Devaux B, Franzen R, Geffer M, Hsu D, Pallard X;
PI Rotbard J, Samsom M, Shi J, Smilek D;
DR MPI; 96-230552/23.
PT Myelin basic derived peptide(s) and analogs - used in the treatment
PS of Multiple Sclerosis, psoriasis, Graves Disease, etc.
PS Example 9; Fig 1; 91pp; English.
CC This sequence represents the human myelin oligodendrocyte protein (MOG).
CC Immunisation with MOG (or the peptide fragments shown in R95375-R95385)
CC can be used to induce experimental allergic encephalomyelitis (EAE) in
CC susceptible strains of mice. EAE is a CD4+ T-cell mediated autoimmune
CC disease which results in demyelination of the central nervous system,
CC resulting in paralysis and other neurological abnormalities. EAE is a
CC commonly used animal model for human multiple sclerosis (MS). These
CC sequences can be used in compositions for treating MS in a mammal. The
CC composition acts to down regulate the autoimmune response, and may be
CC administered in an amount sufficient to prevent the onset of symptoms of
CC MS. The compositions may also be used to treat advanced stage MS,
CC especially relapsing-remitting MS, chronic progressive MS or benign MS.
CC These peptides may also be used in the treatment of other diseases
CC involving myelin autoantigens, including diabetes, Graves disease,
CC myasthenia gravis, Good Pasture's syndrome, psoriasis, thyroiditis, and
CC rheumatoid arthritis. Peptides derived from other myelin autoantigens,
CC such as myelin basic protein (MBP, see R95334-R95374), proteolipid
CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as
CC alternatives to the MOG peptides in these compositions.
SO Sequence 170 AA;

Query Match 99.5%; Score 917; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 1e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDGTILDSIGRFGDGDGAPRSGSKD 61
DB 1 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDGTILDSIGRFGDGDGAPRSGSKD 60

DE Foetal myelin basic protein MBP+X2Cys81/bact.
 KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
 KM multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KM T-lymphocyte; T-cell; anergy; apoptosis.
 OS Synthetic.
 FH Key
 FT region
 FT Location/Qualifiers
 FT 60..85
 FT /label=x2
 FT /note="exon 2-encoded region"
 PN MO9634622-A1.
 PD 07-NOV-1996.
 PE 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pellfrey CM, Squinto SP, Wilkins JA;
 DR N-PSDB; T41897.
 DR WPI; 96-505898/50.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis; Page 81-82; 156pp; English.
 PS A 21.5 kDa foetal isoform (W06107) of myelin basic protein,
 CC MBP+X2Cys81/bact., is the product of a DNA construct (T41896)
 CC based on the human foetal MBP+X2Cys81 isoform (W00399) but
 CC utilizing bacterially-preferred codons in place of the native human
 CC codons (see also T41889). This increases prodn. of the MBP in E.
 CC coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also
 CC W00399 and W06108) are useful in the clinical assessment, diagnosis
 CC and treatment of MS.
 SQ Sequence 203 AA;

Query Match 97.5%; Score 899; DB 1; Length 203;
 Best local Similarity 86.8%; Pred. No. 1e-87;
 Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MASQKRPDSQHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFFGGDGAAPKRSKG-- 58
 DB 1 MASQKRPDSQHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFFGGDGAAPKRSKGKV 60

QY 59 -----KDSHHPARTAHYGSLPQKSHGRTQDENPVVHFEKNI 94
 DB 61 PWLKPGHSPLPSSARSGPGLCNMYKDSHHPARTAHYGSLSLQKSHGRTQDENPVVHFEKNI 120

QY 95 VTPTPTPPSGQKRGSLSRFSWGAEGORPGFGYGRASDYKSAHKGFGVDAQGLTSKI 154
 DB 121 VTPTPTPPSGQKRGSLSRFSWGAEGORPGFGYGRASDYKSAHKGFGVDAQGLTSKI 180

QY 155 FKLGGRDSRSGSPMARR 171
 DB 181 FKLGGRDSRSGSPMARR 197

RESULT 8
 W06108
 ID W06108 standard; Protein; 203 AA.
 AC W06108;
 DT 01-FEB-1997 (first entry)
 DE Foetal myelin basic protein MBP+X2Ser81/bact.
 KM Myelin basic protein; MBP; MBP+X2Ser81; proteolipid protein; PLP;
 KM multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KM T-lymphocyte; T-cell; anergy; apoptosis.
 OS Synthetic.
 FH Key
 FT region
 FT Location/Qualifiers
 FT 60..85
 FT /label=x2
 FT /note="exon 2-encoded region, with Cys81Ser
 FT mutation"
 FT 198..203
 FT peptide

FT FT /label= Hexa-histidine_tag
 FT FT /note= "the hexa-histidine tag facilitates
 FT FT purification of the recombinant protein
 FT FT from host cells"
 PN MO9634622-A1.
 PD 07-NOV-1996.
 PE 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pellfrey CM, Squinto SP, Wilkins JA;
 DR N-PSDB; T41897.
 DR WPI; 96-505898/50.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis; Page 82-83; 156pp; English.
 PS A 21.5 kDa foetal isoform (W06108) of myelin basic protein,
 CC MBP+X2Ser81/bact., is the product of a DNA construct (T41897)
 CC based on the human foetal MBP+X2Cys81 isoform (W00399) but
 CC utilizing codons that are highly expressed in bacterial genes in
 CC place of the native codons (see also T41889) and incorporating a
 CC sequence coding for a hexa-histidine tail. This allows large-
 CC scale prodn. and purification of the MBP in bacterial hosts.
 CC Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) are
 CC useful in the clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 203 AA;

Query Match 97.5%; Score 899; DB 1; Length 203;
 Best local Similarity 86.8%; Pred. No. 1e-87;
 Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MASQKRPDSQHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFFGGDGAAPKRSKG-- 58
 DB 1 MASQKRPDSQHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFFGGDGAAPKRSKGKV 60

QY 59 -----KDSHHPARTAHYGSLPQKSHGRTQDENPVVHFEKNI 94
 DB 61 PWLKPGHSPLPSSARSGPGLCNMYKDSHHPARTAHYGSLSLQKSHGRTQDENPVVHFEKNI 120

QY 95 VTPTPTPPSGQKRGSLSRFSWGAEGORPGFGYGRASDYKSAHKGFGVDAQGLTSKI 154
 DB 121 VTPTPTPPSGQKRGSLSRFSWGAEGORPGFGYGRASDYKSAHKGFGVDAQGLTSKI 180

QY 155 FKLGGRDSRSGSPMARR 171
 DB 181 FKLGGRDSRSGSPMARR 197

RESULT 9
 W06103
 ID W06103 standard; Protein; 373 AA.
 AC W06103;
 DT 01-FEB-1997 (first entry)
 DE MP4 chimera (MBP21.5-delta PLP4 fusion).
 KM Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
 KM MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KM therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.
 OS Synthetic.
 FH Key
 FT protein
 FT Location/Qualifiers
 FT 1..368
 FT /note="preferred protein of the invention"
 FT 1..197
 FT domain
 FT /label= MBP21.5
 FT peptide
 FT 198..200
 FT /label= Spacer
 FT domain
 FT 201..373
 FT /label= Delta_PLP4
 FT 201..205
 FT peptide

FT	/note= "synthetic N-terminal peptide not found in
FT	the native protein"
FT	208. . 219
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	210. . 230
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	241. . 261
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	242. . 259
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	244. . 257
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	248. . 269
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	256. . 269
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	257. . 269
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	268. . 281
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	270. . 303
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	292. . 304
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	292. . 307
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	295. . 306
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	314. . 326
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	326. . 337
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	326. . 339
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	351. . 365
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	213. . 234
FT	/label= Epitope
FT	/note= "PLP epitope associated with MS"
FT	213. . 234
FT	/label= Epitope
FT	/note= "encephalitogenic epitope in mouse model"
FT	256. . 269
FT	/label= Epitope
FT	/note= "encephalitogenic epitope in mouse model"
FT	292. . 304
FT	/label= Epitope
FT	/note= "encephalitogenic epitope in mouse model"
FT	369. . 373
FT	/label= Histidine tag
FT	/note= "hexa-histidine tag facilitates recombinant
FT	protein purification"
FT	protein purification"
PD	W09634622-A1.
PD	07-NOV-1996.
PF	22-APR-1996; U05611.
PR	02-MAY-1995; US-431648.
PR	02-MAY-1995; US-431644.
PR	07-JUN-1995; US-482114.
PA	(ALEX-) ALEXION PHARM INC.

PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PI	Lernardo M., Mats L, McFarland HF, Mueller EE, Mueller JP;
PI	Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
DR	WFLI: 96-505898/50.
DR	N-PDSB: T41893.
PT	New human myelin basic protein and proteolipid protein variant(s) -
PT	used in the assessment, diagnosis and treatment of multiple
PT	sclerosis
PS	Claim 34: Page 110-112; 156pp: English.
CC	MP4 chimera (W06103) is a fusion protein composed of human myelin
CC	basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and
CC	delta PLP4 (W06101), a proteolipid protein (PLP) mutein that lacks
CC	all 4 hydrophobic domains of native human PLP (W06106) but
CC	includes PLP epitopes associated with multiple sclerosis (MS). It
CC	can be expressed in E. coli transformants using a DNA construct
CC	(T41893) convey. the MBP21.5-delta PLP4 gene fusion. MP4 chimera
CC	and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)
CC	are useful for the clinical assessment, diagnosis and treatment
CC	of MS.
SQ	Sequence 373 AA;
Query Match	97.5%; Score 899; DB 1; Length 373;
Best Local Similarity	86.8%; Pred. No. 2,2e+87;
Matches 171; Conservative	0; Mismatches 0; Indels 26; Gaps 1.
QY	1 MASQRPSQRHGSKYLATASTMDHARHGFLPRHRDTGLDLSIGREFGGDGAPKRGSG-- 58
Dd	1 MASGRPSQRHGSKLYLATASTMDHARHGFLPRHRDTGLDLSIGREFGGDGAPKRGSGKV 60
QY	59 -----KDSHHPARTAYGSLSPQKSHRRTQDENRVVHFVKNI 94
Dd	61 PWLKGRSPLPSHAHQOGELCNMYDSHHPATATAYGSIPQKSHRRTQDENRVVHFVKNI 120
QY	95 VTPRPSPSQCKGRGLSLSRFSWGAEQGRPGGYGGRASDYSAKKGFGVAGOGTLSKI 154
Dd	121 VTFRPPSPSQCKGRGLSLSRFSWGAEQGRPGGYGGRASDYSAKKGFGVADGTLSKI 180
QY	155 FKLGRDSRSSGSPMAR 171
Dd	181 FKLGRDSRSSGSPMAR 197
RESULT 10	
W06102	W06102 standard; Protein; 385 AA.
ID	W06102:
AC	01-FEB-1997 (first entry)
DE	MP3 chimera (MBP21.5-delta PLP3 fusion).
KM	Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
RW	MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
KW	therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.
OS	Synthetic.
FH	Key
FT	domain location/qualifiers
FT	peptide 1..197
FT	198..200 /label= MBP21.5
FT	/label= Spacer
FT	201..385 /label= Delta_PLP3
FN	WO9634622-A1.
PD	07-NOV-1996.
PE	22-APR-1996; U05611.
PR	02-MAY-1995; US-431648.
PR	02-MAY-1995; US-431644.
PR	07-JUN-1995; US-482114.
PA	(ALEX-) ALEXION PHARM INC.
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PI	Lernardo M., Mats L, McFarland HF, Mueller EE, Mueller JP;
PI	Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
DR	WFLI: 96-505898/50.
DR	N-PDSB: T41892.
PT	New human myelin basic protein and proteolipid protein variant(s) -

PT used in the assessment, diagnosis and treatment of multiple
 PT Sclerosis
 PS Claim 33: Page 108-110; 156pp; English.
 CC MP3 chimera (W06102) is a fusion protein composed of human myelin
 basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and
 delta PLP3 (W00400), a proteolipid protein (PLP) mutain that lacks
 hydrophobic domains 1, 3 and 4 of native human PLP (W06106) but
 includes PLP epitopes associated with multiple sclerosis (MS). It
 can be expressed in E. coli transformants using a DNA construct
 (T41892) contg. the MBP21.5-delta PLP3 gene fusion. MP3 chimera
 CC and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)
 CC are useful for the clinical assessment, diagnosis and treatment
 CC of MS.
 SQ Sequence 385 AA:

Query Match 97.5%; Score 899; DB 1; Length 385;
 Best Local Similarity 86.8%; Pred. No. 2.3e-87;
 Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MASOKRPSQHGSKYLATASTMDHARHGFPLPRHDTGILDSIGREFGCDRGAPKRGSG-- 58
 |||||||
 Db 1 MASOKRPSQHGSKYLATASTMDHARHGFPLPRHDTGILDSIGREFGCDRGAPKRGSGKV 60
 QY 59 -----KDSHPARTAHYGSILPKSHGRTQDENPVVHFVKNI 94
 |||||||
 Db 61 PWLKGPSPLPSHARSQPLCNMYKDSHPARTAHYGSILPKSHGRTQDENPVVHFVKNI 120
 QY 95 VMPPRPSPGSGRGSLSRFSWGAEGORPGFGYGRASAHKGFQVDAQGLSKI 154
 |||||||
 Db 121 VMPPRPSPGSGRGSLSRFSWGAEGORPGFGYGRASAHKGFQVDAQGLSKI 180
 QY 155 FKUGRDSRSGSPMAR 171
 |||||||
 Db 181 FKUGRDSRSGSPMAR 197

RESULT 11
 W06105
 ID W06105 standard; Protein; 492 AA.
 AC W06105:
 DT 01-FEB-1997 (first entry)
 DE MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion).
 KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;
 MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KW therapy; T-lymphocyte; T-cell; MMOGP4 chimera;
 KW myelin oligodendrocyte glycoprotein; MOG.
 OS Synthetic.
 FH Key
 FT Location/Qualifiers
 FT 1..487
 FT /note= "preferred protein of the invention"
 FT domain
 FT 1..197
 FT /label= MBP21.5
 FT domain
 FT 198..319
 FT /label= MOG
 FT /note= "MOG extracellular domain"
 FT domain
 FT 320..486
 FT /label= Delta_PLP4
 FT region
 FT 327..338
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 329..349
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 360..380
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 361..278
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 363..376
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 363..376
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"

FT region
 FT 367..378
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 375..388
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 376..388
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 387..400
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 389..402
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 411..423
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 411..426
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 414..425
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 433..445
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 445..456
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 445..458
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 470..484
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 375..388
 FT /label= Epitope
 FT /note= "encephalitogenic epitope in mouse model"
 FT region
 FT 411..423
 FT /label= Epitope
 FT /note= "encephalitogenic epitope in mouse model"
 FT peptide
 FT 487..492
 FT /label= Histidine tag
 FT /note= "hexa-histidine tag facilitates recombinant
 FT protein purification"
 FT W0634622-A1.
 PN 07-NOV-1996.
 PD 22-APR-1996; U05611.
 PE 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo M, Mats L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Palfrey CM, Squinto SP, Walkins JA;
 DR WPI. 96-505898/50.
 DR N-PEDB: T41893.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 36: Page 115-117; 156pp; English.
 CC MMOGP4 chimera (W06105) is a fusion protein composed of human myelin
 basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the
 CC extracellular domain of human myelin oligodendrocyte glycoprotein
 CC (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutain.
 CC MBP21.5, PLP and MOG are all recognised by autoreactive T cells from
 CC multiple sclerosis (MS) patients. The chimera was produced using the
 CC a DNA construct (T41893) obtd. by inserting a sequence encoding the
 CC MOG moiety into MP4 chimera DNA (see also T41893). MMOGP4 chimera

CC can be expressed in bacterial cell hosts. PLP and MBP polypeptides
 CC (see also W00400, W06101-04, W06107-08) are useful in the clinical
 CC assessment, diagnosis and treatment of MS.
 SQ Sequence 492 AA;

Query Match 97.5%; Score 899; DB 1; Length 492;

Best Local Similarity 86.8%; Pred. No. 3e-87; Mismatches 0; Indels 26; Gaps 1;

Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

DB 61 PWLPGSRPLPSHARSOPGLCNMYKDSHHPARTAHYGSLLPKSHQRTDENPVVHFFKNI 120

QY 95 VTPRTPPSOGKRGSLSTRSGWGAEGORPGFGYGRASDYKSAHKFGYDAOGTLSKI 154

DB 121 VTPRTPPSOGKRGSLSTRSGWGAEGORPGFGYGRASDYKSAHKFGYDAOGTLSKI 180

QY 155 FKLGGRDSRSGSPMAR 171

DB 181 FKLGGRDSRSGSPMAR 197

RESULT 12

W06104

ID W06104 standard: protein; 375 AA.

AC W06104;

DT 01-FEB-1997 (first entry)

DE PM4 chimera (delta PLP4-MBP21.5 fusion).

KM Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

KM therapy: T-lymphocyte; T-cell; PM4 chimera.

OS Synthetic.

PH Key

FT protein

FT /note= "preferred PM4 chimera protein"

FT domain

FT 1.169

FT /label= Delta-PLP4

FT peptide

FT 1.15

FT /note= "synthetic N-terminal peptide not found in the native protein"

FT region

FT 9.20

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 11.31

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT region

FT 42.62

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 43.60

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT region

FT 45.58

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 49.70

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT region

FT 57.70

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 58.71

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT region

FT 69.82

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT region

FT 71.104

FT /note= "PLP epitope associated with MS"

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 93.105

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 93.108

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 96.107

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 115.127

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 127.138

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 127.140

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 152.166

FT /label= Eptope

FT /note= "PLP epitope associated with MS"

FT 14.35

FT /label= Eptope

FT /note= "encephalitogenic epitope in mouse model"

FT 57.70

FT /label= Eptope

FT /note= "encephalitogenic epitope in mouse model"

FT 93.105

FT /label= Eptope

FT /note= "encephalitogenic epitope in mouse model"

FT 170.173

FT /label= Spacer

FT 174.368

FT /label= MBP21.5

FT 369.375

FT /label= Histidine tag

FT /note= "hexa-histidine tag facilitates recombinant protein purification"

W0634623-A1.

PD 07-NOV-1996.

PE 22-APR-1996; U05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Leonardo MJ, Matlis L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

DR WPI: 96-505898/50.

DR N-PSDB: T41894.

PT New human myelin basic protein and proteolipid protein variant(s) -

PT used in the assessment, diagnosis and treatment of multiple

PT sclerosis

PS Claim 35; Page 113-114; 156pp; English.

CC PM4 chimera (W06104) is a fusion protein composed of delta PLP4

CC (W06101) and MBP21.5 (W00399). Delta PLP4 is a proteolipid protein

CC (PLP) myelin that lacks all 4 hydrophobic domains of native human

CC PLP (W06106) but includes PLP epitopes associated with multiple

CC sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic

CC protein (MBP) associated with MS. PM4 is in reverse orientation to

CC MP4 chimera (W06103). It can be expressed in bacterial host cells

CC using a DNA construct (T41894). PLP polypeptides (see also W00400,

CC W06101-03 and W06105) can be used in the clinical assessment,

CC diagnosis and treatment of MS.

SQ Sequence 375 AA;

Query Match 97.0%; Score 894; DB 1; Length 375;

Best Local Similarity 86.7%; Pred. No. 7.4e-87; Mismatches 0; Indels 26; Gaps 1;

Matches 170; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

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QY 2 ASOKRPSQRHSGKYLTASTMDHARHGFLPRHNDTGILDSIGRFFGGDGRAPKRGSG---58
DB 174 ASOKRPSQRHSGKYLTASTMDHARHGFLPRHNDTGILDSIGRFFGGDGRAPKRGSGKYP 233
QY 59 -----KDSHHPARTAHYGSLPQKSGHRTQDENPVVHFFKNIT 95
DB 234 WLKPGSRPLPSHARSQPGCLCMYKDSHHPARTAHYGSLPQKSGHRTQDENPVVHFFKNIT 293
QY 96 TPRTPPPSQGGKRGSLSRFSWGAEGORPGFGYGRASDYKSAHKGFQVDAQGLTSKIF 155
DB 294 TPRTPPPSQGGKRGSLSRFSWGAEGORPGFGYGRASDYKSAHKGFQVDAQGLTSKIF 353
QY 156 KLGGRDSRSGSPMAR 171
DB 354 KLGGRDSRSGSPMAR 369

RESULT 13
R30736
ID R30736 standard; Protein: 170 AA.
AC R30736;
DT 21-MAY-1993 (first entry)
DE Human MBP.
KW Acetylcholine receptor; MHC; myelin basic protein; MBP.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 1
FT modified_site /note="N-Ac-Ala"
FT modified_site 107
FT modified_site /note="Me-Arg"
FT peptide 1..14
FT /note="claim 30; page 68"
PN WO9218150-A.
PD 29-OCT-1992.
PF 23-APR-1992; U03391.
PR 23-APR-1991; US-690840.
PA (ANER-) ANERGEN INC.
PI Clark BR, Lerch BL, Sharma SD;
DR MPI; 93-036056/04.
PT Pure major MHC-peptide complex - useful in treating deleterious
PS immune response such as autoimmunity
PS Claim 30; Page 68 + Fig 7; 93pp; English.
CC A method is claimed for the prepn. of a pure major MHC-peptide
CC complex. The MHC component is a Class II glycoprotein of the MHC
CC and the peptide comprises amino acids 1-14 of MBP.
SQ Sequence 170 AA;

Query Match 96.6%; Score 891; DB 1; Length 170;
Best Local Similarity 98.2%; Pred. No. 5,9e-87;
Matches 167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ASOKRPSQRHSGKYLTASTMDHARHGFLPRHNDTGILDSIGRFFGGDGRAPKRGSGKDS 61
DB 1 ASOKRPSQRHSGKYLTASTMDHARHGFLPRHNDTGILDSIGRFFGGDGRAPKRGSGKDS 60
QY 62 HHPARTAHYGSLPQKSGHRTQDENPVVHFFKNITVPTPPPSQGGKRGSLSRFSWGAEG 121
DB 61 HHPARTAHYGSLPQKSGHRTQDENPVVHFFKNITVPTPPPSQGGKRGSLSRFSWGAEG 120
QY 122 QRRGFGYGRASDYKSAHKGFQVDAQGLTSKIFKLGGRDSRSGSPMAR 171
DB 121 QRRGFGYGRASDYKSAHKGFQVDAQGLTSKIFKLGGRDSRSGSPMAR 170

RESULT 14
R04717
ID R04717 standard; Protein: 168 AA.
AC R04717;
DT 23-AUG-1990 (first entry)
DE Empirically determined sequence of myelin basic protein (MBP)
KW Myelin basic protein; multiple sclerosis; autoantigen; autoimmune disease;
KW epitope; myelin sheath.

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FH Key Location/Qualifiers
FT misc_difference 1
FT /label=OTHER
FT /note="N-Ac-Ala"
FT misc_difference 168
FT /label=OTHER
FT /note="Arg-COOH"
PN WO8912459-A.
PD 28-DEC-1989.
PF 23-JUN-1989; U02784.
PR 21-JUN-1989; US-367751, US-210594.
PA (BIOS-) Biospan Corp.
PI Sharma SD, Lerch LB, Clark BR;
DR MPI; 90-022384/03.
PT New complexes of histo-compatible glyco:protein -
PT with antigenic peptide(s) and label or toxin, used to target
PT antigen specific T helper cells
PS Fig 7; 74pp; English.
CC The patent claims complexes of formulae (I), (II) and (III) which are as
CC follows: (I) X - MCH - peptide; (II) MHC - peptide - X; (III) MHC -
CC peptide. Where X - toxin or labelling sp.; MHC - effective portion of the
CC major histocompatibility glycoprotein; and the peptide includes an
CC epitope associated with one of the major autoimmune diseases, including
CC multiple sclerosis (MS). MBP is the principle autoantigen in MS and is a
CC candidate peptide for insertion in the complexes which can be used to
CC treat and monitor MS. Pertinent sections of MBP are determined
CC empirically, using a strain of mice which develops experimental
CC allergic encephalitis when immunised with bovine MBP. The sequence
CC given in p94717 is with the substitution of the residues above the
CC sequence in Fig 7. The sequence without substitutions is given in p92226.
SQ Sequence 168 AA;

Query Match 92.7%; Score 855; DB 1; Length 168;
Best Local Similarity 96.5%; Pred. No. 3,7e-83;
Matches 164; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 2 ASOKRPSQRHSGKYLTASTMDHARHGFLPRHNDTGILDSIGRFFGGDGRAPKRGSGKDS 61
DB 1 ASOKRPSQ-HG-KYLTASTMDHARHGFLPRHNDTGILDSIGRFFGGDGRAPKRGSGKDS 58
QY 62 HHPARTAHYGSLPQKSGHRTQDENPVVHFFKNITVPTPPPSQGGKRGSLSRFSWGAEG 121
DB 59 HHPARTAHYGSLPQKSGHRTQDENPVVHFFKNITVPTPPPSQGGKMGSLSRFSWGAEG 118
QY 122 QRRGFGYGRASDYKSAHKGFQVDAQGLTSKIFKLGGRDSRSGSPMAR 171
DB 119 QRRGFGYGRASDYKSAHKGFQVDAQGLTSKIFKLGGRDSRSGSPMAR 168

RESULT 15
R48594
ID R48594 standard; Protein: 168 AA.
AC R48594;
DT 31-JUL-1994 (first entry)
DE Rabbit myelin basic protein.
KW Proteolipid protein; myelin basic protein; retrovirus;
KW neurological disease; by-stander antigen; TGF-beta;
KW transforming growth factor-beta; T-cell; T-lymphocyte;
KW myelopathy; paraparesis; human immunodeficiency virus type 1.
OS Oryctolagus cuniculus.
PN WO9404121-A.
PD 03-MAR-1994.
PF 17-AUG-1993; U07786.
PR 17-AUG-1992; US-931217.
PA (AUTO-) AUTOIMMUNE INC.
PI Hafner DA, Weiner HL;
DR MPI; 94-082786/10.
PT Treating retroviral associated neurological disease - by admin.
PT of by-stander antigen, causing release of transforming growth
PT factor beta from suppressor T cells
PS Disclosure: Page 49; 64pp; English.
SQ Myelin basic proteins (sequences R48592-96) and cattle proteolipid

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CC protein(R48592) elicit the release of TGF-beta from suppressor T
CC cells and target the T-cells to neural tissue under cytotoxic
CC attack, thereby reducing neurological disease, e.g. HTLV-1
CC associated myelopathy, tropical spastic paraparesis and HIV
CC infection.
SQ Sequence 168 AA;

SQ Sequence 168 AA;

Query Match	90.2%	Score 832;	DB 1;	Length 168;
Best Local Similarity	91.2%	Pred No.	1e-80;	
Matches 155;	Conservative	4;	Mismatches 9;	Indels 2;
				Gaps 1;

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0y 2 ASOKPSPORHSGKYATATSTMDAHARHG/LPHRPTGTJLDSIGREGGDRAPKRGSKDS 61
db 1 ASOKPSPORHSGKYATATSTMDAHARHG/LPHRPTGTJLDSIGRESSDRAPKRGSKD- 59
0y 62 HHPARTAHGSLPOKSHGRTODENPVYEFFKNITVPTPTPSPCKGKGLSTSRFSWAGC 121
db 60 -HAATTHYGSIPKSHSRPDODENPVYEFFKNITVPTPTPSPCKGKGLVLSRFSWAGC 118
0y 122 QRPFGYGRASDYKSAHKGFPGVDAOGTSLKIFKLGGRDSRSGSPPAR 171
db 119 QKPGYGRADYKSAHKGLGADAOGLTSLRKLKLGGRDSRSGSPPAR 166

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Job time: 5855 sec

